

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 23:37:38 ; Search time 14585 Seconds  
(without alignments)  
19967.524 Million cell updates/sec

Title: US-10-005-469-1

Perfect score: 7992

Sequence: 1 gccagcccccgttgggggc.....ctcttcgcagatcaagtact 7992

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	795.4	10.0	935	7	CK284786 EST747508
2	794	9.9	804	7	CK291519 EST754233
3	794	9.9	856	7	CK287297 EST750019
4	794	9.9	910	7	CK287930 EST750652
5	794	9.9	933	7	CK291799 EST754513
6	794	9.9	936	7	CK256977 EST740614
7	794	9.9	947	7	CK298208 EST760922
8	794	9.9	954	7	CK283361 EST746083
9	778.8	9.7	811	7	CK288185 EST750907
10	587	7.3	878	7	CK288711 EST751433
11	577.4	7.2	789	8	AQ361914 mgxb0005K
12	559.8	7.0	620	8	AQ398387 mgxb0009J
13	542.4	6.8	549	7	CK801630 NF32c08f4
14	514.8	6.4	581	8	AQ447874 mgxb0012I
15	508	6.4	509	8	AQ447775 mgxb0011E
16	505.4	6.3	637	8	AQ447230 mgxb0023E
17	503.8	6.3	592	8	AQ449162 mgxb0026P
18	499	6.2	498	8	AQ398880 mgxb0006G
19	496.4	6.2	498	8	AQ398730 mgxb0009G
20	477.4	6.0	586	7	CK801096 NF15h06f4
21	475.8	6.0	857	8	AQ875013 V12088 mt
22	474.8	5.9	710	8	BH972732 odj46h10.
23	469.8	5.9	473	8	AQ397768 mgxb0001J
24	468.8	5.9	594	8	AQ397253 mgxb0003C

C 25	465.2	5.8	850	8	AQ875052	AQ875052 V120F5 mt
C 26	463.4	5.8	798	8	AQ876139	AQ876139 V133G10 m
C 27	458.8	5.7	482	1	AL449872	AL449872 AL449872
C 28	456.8	5.7	861	8	AQ875040	AQ875040 V120E4 mt
C 29	455.6	5.7	815	8	AQ876134	AQ876134 V133F5 mt
C 30	451.2	5.6	799	8	AQ876220	AQ876220 V152G7 mt
C 31	450	5.6	784	8	AQ876152	AQ876152 V133H12 m
C 32	444.6	5.6	790	8	AQ875904	AQ875904 V130H11 m
C 33	437.2	5.5	797	8	AQ876297	AQ876297 V153G3 mt
C 34	434.6	5.4	765	7	CK283362	CK283362 EST746084
C 35	426.8	5.3	804	8	AQ876080	AQ876080 V133A4 mt
C 36	422.8	5.3	759	7	CK298209	CK298209 EST760923
C 37	414.6	5.2	791	8	AQ876019	AQ876019 V132C3 mt
C 38	409.4	5.1	748	8	AQ501530	AQ501530 V20F6 mTn
C 39	408	5.1	635	8	AQ447643	AQ447643 mgxb0008M
C 40	408	5.1	656	8	AQ447140	AQ447140 mgxb0005I
C 41	404	5.1	790	8	AQ875912	AQ875912 V130H8 mt
C 42	404	5.1	791	8	AQ876201	AQ876201 V152E2 mt
C 43	402.6	5.0	856	8	AQ875050	AQ875050 V120F2 mt
C 44	401.8	5.0	760	7	CK287931	CK287931 EST750653
C 45	398.8	5.0	722	6	CD641598	CD641598 AGENCOURT

## ALIGNMENTS

RESULT 1  
CK284786  
LOCUS  
DEFINITION  
EST747508 Nicotiana benthamiana mixed tissue cDNA library, linear EST 02-AUG-2004  
normalized, full-length Nicotiana benthamiana cDNA clone NBMAQ41 5',  
end, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CK284786  
CK284786.1 GI:39858698  
EST.  
Nicotiana benthamiana  
Nicotiana benthamiana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamiales; Solanales; Solanaceae; Nicotiana.

REFERENCE  
AUTHORS  
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,  
Staskiewicz, B., Jin, H. and Baker, B.

TITLE  
JOURNAL  
COMMENT  
Generation of EST sequences from Nicotiana benthamiana  
Other ESTs: EST747509  
Contact: Robin Buell

The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potato-array@tigr.org

Clones can be requested from the University of Arizona Genomics  
Institute via http://genome.arizona.edu/orders/

Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES  
source  
Location/Qualifiers  
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/organism="Nicotiana benthamiana"

/mol\_type="mRNA"

/db\_xref="taxon:4100"

/clone="NBMAQ41"

/tissue\_type="abiotic and biotic stress-treated leaves,"

callus tissue and root tissue"

/lab\_host="DH10B-TonA"

/clone\_lib="Nicotiana benthamiana mixed tissue cDNA

library, normalized, full-length"

/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;

tissues that include callus, roots from liquid culture

grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),

cold-stressed leaves (5 C 3 hr, 6hr), and pathogen

challenged leaves (Pseudomonas syringae pv tomato 12 hr;

Xanthomonas campestris pv campestris 12 hr, 18hr;

Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas

campestris pv vesicatoria 18hr). RNA was isolated from

these tissues and pooled in approximately equal molar amounts."

ORIGIN		Query Match		Best Local Similarity		Matches		Conservative		Mismatches		Indels		Gaps	
10.0%; Score 795.4; DB 7; Length 935;		99.9%; Pred. NO. 1.8e-174;		0;		0;		1;		0;		0;		0;	
386 CATGATTGAACAGATGATTCACGACGAGTTCTCCGCGCTTGGTGGAGAGGCTATT		445													
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446 CGGCTATGACTGGGCAACACAGACATCGGCTGCTGATGCGCGCTTCCGCGCTTC		505													
91 CGGCTATGACTGGGCAACACAGACATCGGCTGCTGATGCGCGCTTCCGCGCTTC		150													
506 AGCGACGGGCGCGGCTTCTTTTGTCAAGACCGACCTGTCGGTGGCCCTGAATGAAT		565													
151 AGCGACGGGCGCGGCTTCTTTTGTCAAGACCGACCTGTCGGTGGCCCTGAATGAAT		210													
566 GCAGGACGAGGACGCGGCTATCGTGGTGGCCACGACGGGGCTTCTTGGCGACTGT		625													
211 GCAGGACGAGGACGCGGCTATCGTGGTGGCCACGACGGGGCTTCTTGGCGACTGT		270													
626 GCTCGACGTTGTCATGACGAGGGAAGGACTGGCTGCTATTGGGGAGTGGCGGGCA		685													
271 GCTCGACGTTGTCATGACGAGGGAAGGACTGGCTGCTATTGGGGAGTGGCGGGCA		330													
686 GGAATCTCTGTCATCTCACTTCTCTCTGCGGAGAAAGTATCCATCATGCTGATGCAAT		745													
331 GGAATCTCTGTCATCTCACTTCTCTCTGCGGAGAAAGTATCCATCATGCTGATGCAAT		390													
746 GCGCGGCTCATACAGCTTTCATCGGCTACTGCTCCCATTCGACCAACGCGAAACATCG		805													
391 GCGCGGCTCATACAGCTTTCATCGGCTACTGCTCCCATTCGACCAACGCGAAACATCG		450													
806 CATCGACGAGCAGCTACTCGATGGAAGCGGCTTGTGATCAGATGATCTGGACGA		865													
451 CATCGACGAGCAGCTACTCGATGGAAGCGGCTTGTGATCAGATGATCTGGACGA		510													
866 AGACATCAGGGCTCGCGCGCAGCACTTGTCCGAGGCTCAAGGCGGCGCATGCCGA		925													
511 AGACATCAGGGCTCGCGCGCAGCACTTGTCCGAGGCTCAAGGCGGCGCATGCCGA		570													
926 CCGCGAGGATCTCGTCTGACCCATTCGCGATGCTGCTTGGCGGAATATCATGCTGGA		985													
571 CCGCGATGATCTCGTCTGACCCATTCGCGATGCTGCTTGGCGGAATATCATGCTGGA		630													
986 TGGCGGCTTTCTGGAATTCATGATGCTGCGCGGCTGGTGGCGGACCGCTATCAGGA		1045													
631 TGGCGGCTTTCTGGAATTCATGATGCTGCGCGGCTGGTGGCGGACCGCTATCAGGA		690													
1046 CATAGCGTTGGCTACCCGCTGATTTGCTGAAGAGCTTGGCGGCGGAATGGGCTGACCGCTT		1105													
691 CATAGCGTTGGCTACCCGCTGATTTGCTGAAGAGCTTGGCGGCGGAATGGGCTGACCGCTT		750													
1106 CTTCTGCTTTACGCTATGCGGCTTCCGATTCGAGCGCATCGCTTCTATCGGCTTCT		1165													
751 CTTCTGCTTTACGCTATGCGGCTTCCGATTCGAGCGCATCGCTTCTATCGGCTTCT		810													
1166 TGACGAGTTCTTCTGAG		1182													
811 TGACGAGTTCTTCTGAG		827													
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LOCUS		EST754233		Nicotiana benthamiana mixed tissue cDNA library,											
DEFINITION		normalized, full-length Nicotiana benthamiana cDNA clone NBMC276 5'													
end, mRNA sequence.															
ACCESSION		CK291519													
VERSION		CK291519.1		GI:39872047											

EST.  
Nicotiana benthamiana  
Nicotiana benthamiana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 804)  
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,  
Staskawicz, B., Jin, H. and Baker, B.  
Generation of EST sequences from Nicotiana benthamiana  
Unpublished (2003)  
Contact: Robin Buell  
The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potato-array@tigr.org  
Clones can be requested from the University of Arizona Genomics  
Institute via <http://genome.arizona.edu/orders/>.  
Seq primer: ANT TAG GTG ACA CTA TAG.

FEATURES  
1..804  
Location/Qualifiers  
/organism="Nicotiana benthamiana"  
/mol\_type="mRNA"  
/db\_xref="taxon:4100"  
/clone="NBMC276"  
/tissue\_type="abiotic and biotic stress-treated leaves,  
callus tissue and root tissue"  
/lab\_host="DH10B-TonA"  
/clone\_lib="Nicotiana benthamiana mixed tissue cDNA  
library, normalized, full-length"  
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;  
supplier: RNA was isolated from Nicotiana benthamiana  
tissues that include callus, roots from liquid culture  
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),  
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen  
challenged leaves (Pseudomonas syringae pv tomato 12 hr;  
Xanthomonas campestris pv campestris 12 hr, 18hr;  
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas  
campestris pv vesicatoria 18hr). RNA was isolated from  
these tissues and pooled in approximately equal molar  
amounts."

ORIGIN  
Query Match 9.9%; Score 794; DB 7; Length 804;  
Best Local Similarity 100.0%; Pred. NO. 3.7e-174; Indels 0; Gaps 0;  
Matches 794; Conservative 0; Mismatches 0;  
389 GATTGAACAAGATGATTCACGACGAGTTCTCCGCGCGCTTGGTGGAGAGGCTATTCCG 448  
2 GATTGAACAAGATGATTCACGACGAGTTCTCCGCGCGCTTGGTGGAGAGGCTATTCCG 61  
449 CTATGACTGGGCAACACAGACAAATCGGCTGCTCTGATGCCCGCGCTTCCGCGCTCAGC 508  
62 CTATGACTGGGCAACACAGACAAATCGGCTGCTCTGATGCCCGCGCTTCCGCGCTCAGC 121  
509 GCAGGGGCGCGGCTTCTTTTGTCAAGACGACCTGTCGCGTGCCTGGAATGAATGCA 568  
122 GCAGGGGCGCGGCTTCTTTTGTCAAGACGACCTGTCGCGTGCCTGGAATGAATGCA 181  
569 GCAGGAGGACGCGGCTATCGTGGCTGCCACGACGCGGCGTTCCTTCCGAGCTGTGCT 628  
182 GCAGGAGGACGCGGCTATCGTGGCTGCCACGACGCGGCGTTCCTTCCGAGCTGTGCT 241  
629 GCAGCTTGTCACTGAAGCGGGAAGGACTGGCTGCTATTTGGCGAAGTCCCGGGCAGGA 688  
242 CGACGTTGTCACTGAAGCGGGAAGGACTGGCTGCTATTTGGCGAAGTCCCGGGCAGGA 301  
689 TCTCTGTCTCATCTCACTTGTCTCCGAGAAAGTATCCATCATGGCTGTATGCAATGCG 748  
302 TCTCTGTCTCATCTCACTTGTCTCCGAGAAAGTATCCATCATGGCTGTATGCAATGCG 361  
749 GCGGCTGTCATAGCTTGTATCCGCTACCTGCGCATTCGACCAACGAGCAACATGCGAT 808  
362 GCGGCTGTCATAGCTTGTATCCGCTACCTGCGCATTCGACCAACGAGCAACATGCGAT 421



normalized, full-length Nicotiana benthamiana cDNA clone NBMC75 5',  
end, mRNA sequence.

ACCESSION CK287930  
VERSION CK287930.1 GI:39864940

KEYWORDS EST.

SOURCE Nicotiana benthamiana

ORGANISM Nicotiana benthamiana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE 1 (bases 1 to 910)

AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,

Staskawicz, B., Jin, H. and Baker, B.

TITLE Generation of EST sequences from Nicotiana benthamiana

JOURNAL Unpublished (2003)

COMMENT Other ESTs: EST750653

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from the University of Arizona Genomics

Institute via http://genome.arizona.edu/orders/

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

1..910

/organism="Nicotiana benthamiana"

/mol\_type="mRNA"

/db\_xref="taxon:4100"

/clone="NBMC75"

/tissue\_type="abiotic and biotic stress-treated leaves,

callus tissue and root tissue"

/lab\_host="DH10B-Tona"

/clone\_lib="Nicotiana benthamiana mixed tissue cDNA

library, normalized, full-length"

/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;

supplier: RNA was isolated from Nicotiana benthamiana

tissues that include callus, roots from liquid culture

grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),

cold-stressed leaves (5 C 3 hr, 6hr), and pathogen

challenged leaves (Pseudomonas syringae pv tomato 12 hr;

Xanthomonas campestris pv campestris 12 hr, 18hr;

Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas

campestris pv vesicatoria 18hr). RNA was isolated from

these tissues and pooled in approximately equal molar

amounts."

ORIGIN

Query Match 9.9%; Score 794; DB 7; Length 910;

Best Local Similarity 100.0%; Pred. No. 3.8e-174;

Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

389 GATTGAACAAGATGATGACGAGGTTCTCCGCCCGCTGGGTGGAGAGGCTATTCGG 448

4 GATTGAACAAGATGATGACGAGGTTCTCCGCCCGCTGGGTGGAGAGGCTATTCGG 63

449 CTATGACTGGCAGACAGACAAATCGGCTGCTCTGATGCCCGCGTTCGGCTGTACG 508

64 CTATGACTGGCAGACAGACAAATCGGCTGCTCTGATGCCCGCGTTCGGCTGTACG 123

509 GCAGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGGCCCTGAATGAATGCA 568

124 GCAGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGGCCCTGAATGAATGCA 183

569 GGACGAGGCGAGCGCGCTATGCTGGTGGCCAGCGGGCTTCCTGGCGAGCTGTGCT 628

184 GGACGAGGCGAGCGCGCTATGCTGGTGGCCAGCGGGCTTCCTGGCGAGCTGTGCT 243

629 CGACGTTGCTACTGAACGGAGGAGGACTGGCTGCTATTGGGCGAAGTGCCTGGGCGAG 688

244 CGACGTTGCTACTGAACGGAGGAGGACTGGCTGCTATTGGGCGAAGTGCCTGGGCGAG 303

689 TCTCTCTCATCTCACCTTCTCTCCGCGAAGATATCCATCATGGCTGATCCATGCG 748

Db TCTCTCTCATCTCACCTTCTCTCCGCGAAGATATCCATCATGGCTGATGCAATCGG 363

Qy GCGGCTGATAGCGTTTATCGGCTACCTCGCCATTTCGACCAACGAGCAACATCGCAT 808

Db GCGGCTGATAGCGTTTATCGGCTACCTCGCCATTTCGACCAACGAGCAACATCGCAT 423

Qy CGAGCGACGATCTACTCGGATGGAAGCCGGTCTTTGCGATCAGGATGATCTGGACGAAGA 868

Db CGAGCGACGATCTACTCGGATGGAAGCCGGTCTTTGCGATCAGGATGATCTGGACGAAGA 483

Qy GCATCAGGGGCTCGCGCCAGCGAACTGTTGCCAGGCTCAAGGCGGCATGCCGACGG 928

Db GCATCAGGGGCTCGCGCCAGCGAACTGTTGCCAGGCTCAAGGCGGCATGCCGACGG 543

Qy CGAGATCTCTGCTGACCCATGGCGATGCGCTTTCGCGAATATCATCGTGGAAATCG 988

Db CGAGATCTCTGCTGACCCATGGCGATGCGCTTTCGCGAATATCATCGTGGAAATCG 603

Qy CCGCTTTTCTGATTCATCGACTGTGGCGGCTGGTGGCGGACCGCTATCAGGACAT 1048

Db CCGCTTTTCTGATTCATCGACTGTGGCGGCTGGTGGCGGACCGCTATCAGGACAT 663

Qy AGCGTTGGCTACCGGTGATATTGCTGAAGAGCTTGGCGGCGAATGGCGCTTCCT 1108

Db AGCGTTGGCTACCGGTGATATTGCTGAAGAGCTTGGCGGCGAATGGCGCTTCCT 723

Qy CGTGCTTTACGATTCGCGCTCCCGATTCGCGAGCGATCGCCCTTCTATCGCCTTCTTGA 1168

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Qy CGAGTTCTTCTGAG 1182

Db CGAGTTCTTCTGAG 797

RESULT 5

CK291799 933 bp mRNA linear EST 02-AUG-2004

LOCUS EST754513 Nicotiana benthamiana mixed tissue cDNA library,

DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NBMC477 5',

end, mRNA sequence.

ACCESSION CK291799

VERSION CK291799.1 GI:39872608

KEYWORDS Nicotiana benthamiana

SOURCE Nicotiana benthamiana

ORGANISM Nicotiana benthamiana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE 1 (bases 1 to 933)

AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,

Staskawicz, B., Jin, H. and Baker, B.

TITLE Generation of EST sequences from Nicotiana benthamiana

JOURNAL Unpublished (2003)

COMMENT Other ESTs: EST754514

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from the University of Arizona Genomics

Institute via http://genome.arizona.edu/orders/

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

1..933

/organism="Nicotiana benthamiana"

/mol\_type="mRNA"

/db\_xref="taxon:4100"

/clone="NBMC477"

/tissue\_type="abiotic and biotic stress-treated leaves,

callus tissue and root tissue"

/lab\_host="DH10B-Tona"

/clone\_lib="Nicotiana benthamiana mixed tissue cDNA

library, normalized, full-length"



Xanthomonas campestris pv campestris 12 hr, 18hr;  
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas  
campestris pv vesicatoria 18hr). RNA was isolated from  
these tissues and pooled in approximately equal molar  
amounts."

ORIGIN

Query Match 9.9%; Score 794; DB 7; Length 947;  
Best Local Similarity 100.0%; Pred. No. 3.9e-174; Indels 0; Gaps 0;  
Matches 794; Conservative 0; Mismatches 0;

QY 389 GATTGAACAAGATGGATTGACGACGAGGTTCTCCCGCCGCTTGGGTGGAGAGCTATTGCG 448  
DB 17 GATTGAACAAGATGGATTGACGACGAGGTTCTCCCGCCGCTTGGGTGGAGAGCTATTGCG 76  
QY 449 CTATGACTGGGCAACAACAGACAATCGGCTGCTTGTATGCGCCGCTGTTCCGGCTGTACGC 508  
DB 77 CTATGACTGGGCAACAACAGACAATCGGCTGCTTGTATGCGCCGCTGTTCCGGCTGTACGC 136  
QY 509 GCAGGGGCGCCGGTCTTTTGTCAAGACCGACCTGTCGGTGCCTTGAATGAATGCA 568  
DB 137 GCAGGGGCGCCGGTCTTTTGTCAAGACCGACCTGTCGGTGCCTTGAATGAATGCA 196  
QY 569 GCAGGAGGCGCGGCTATCGTGGTGGCCACGACGGGCGTTCCTTGGCGAGCTGTGCT 628  
DB 197 GCAGGAGGCGCGGCTATCGTGGTGGCCACGACGGGCGTTCCTTGGCGAGCTGTGCT 256  
QY 629 CGACGTTGTCACTGAAGCGGGAAGGACTGGTGTCTATTGGGCGAGTCCCGGGCAGGA 688  
DB 257 CGACGTTGTCACTGAAGCGGGAAGGACTGGTGTCTATTGGGCGAGTCCCGGGCAGGA 316  
QY 689 TCTCTGTGCTATCTACCTTGTCTTCCGCGAAGATATCCATCATGGCTGATCAATGCG 748  
DB 317 TCTCTGTGCTATCTACCTTGTCTTCCGCGAAGATATCCATCATGGCTGATCAATGCG 376  
QY 749 GCGGCTGCATGACGCTTGTATCCGGCTACCTGCCCATTCGACCAACGAGGAAATCGCAT 808  
DB 377 GCGGCTGCATGACGCTTGTATCCGGCTACCTGCCCATTCGACCAACGAGGAAATCGCAT 436  
QY 809 CGACGAGGACGCTACTCGGATGGAAGCGGCTTGTGCTGATCAGGATGATCTGGACGAAGA 868  
DB 437 CGACGAGGACGCTACTCGGATGGAAGCGGCTTGTGCTGATCAGGATGATCTGGACGAAGA 496  
QY 869 GCATCAGGGGCTCGCGCAGCCGACGCTTGGCAGGCTCAAGCGCGCATGCCCGACGG 928  
DB 497 GCATCAGGGGCTCGCGCAGCCGACGCTTGGCAGGCTCAAGCGCGCATGCCCGACGG 556  
QY 929 CGAGGATCTCGTGTGACCCATGGCGATGCTGCTTCCGGAATATCATGTTGGAAATGG 988  
DB 557 CGAGGATCTCGTGTGACCCATGGCGATGCTGCTTCCGGAATATCATGTTGGAAATGG 616  
QY 989 CCGCTTTTCTGGATTTCAGTCTGTCGGCGGCTGGTGTGGCGGACCGCTATCAGGACAT 1048  
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QY 1049 AGCGTTGGCTACCGCTGATATTGCTGAGAGCTTGGCGGCGGAATGGGCTGACCGTCTCT 1108  
DB 677 AGCGTTGGCTACCGCTGATATTGCTGAGAGCTTGGCGGCGGAATGGGCTGACCGTCTCT 736  
QY 1109 CGTGTCTTACGATTCGCGGCTCCCGATTCGAGCGCATCGCTTCTATCGCTTCTTGA 1168  
DB 737 CGTGTCTTACGATTCGCGGCTCCCGATTCGAGCGCATCGCTTCTATCGCTTCTTGA 796  
QY 1169 CGAGTTCTTCTGAG 1182  
DB 797 CGAGTTCTTCTGAG 810

RESULT 8

CK283361

LOCUS

DEFINITION

CK283361 954 bp mRNA linear EST 02-AUG-2004  
EST746083 Nicotiana benthamiana mixed tissue cDNA library,  
normalized, full-length Nicotiana benthamiana cDNA clone NEMAG50 5'

QY 809 CGAGCGAGCAGTACTCGGATGGAAGCCGCTTGTGTCAGTACGAGTATCTGGACGAAGA 868  
DB 434 CGAGCGAGCAGTACTCGGATGGAAGCCGCTTGTGTCAGTACGAGTATCTGGACGAAGA 493  
QY 869 GCATCAGGGGCTCGCGCAGCCGAACTGTCGCGAGGCTCAAGCGCGCATGCCCGACGG 928  
DB 494 GCATCAGGGGCTCGCGCAGCCGAACTGTCGCGAGGCTCAAGCGCGCATGCCCGACGG 553  
QY 929 CGAGGATCTCGTGTGACCCATGGCGATGCTGCTTGGCGAATATCATGTTGGAAATGG 988  
DB 554 CGAGGATCTCGTGTGACCCATGGCGATGCTGCTTGGCGAATATCATGTTGGAAATGG 613  
QY 989 CCGCTTTTCTGGATTTCAGTCTGTCGGCGGCTGGTGTGGCGGACCGCTATCAGGACAT 1048  
DB 614 CCGCTTTTCTGGATTTCAGTCTGTCGGCGGCTGGTGTGGCGGACCGCTATCAGGACAT 673  
QY 1049 AGCGTTGGCTACCGCTGATATTGCTGAGAGCTTGGCGGCGGAATGGGCTGACCGTCTCT 1108  
DB 674 AGCGTTGGCTACCGCTGATATTGCTGAGAGCTTGGCGGCGGAATGGGCTGACCGTCTCT 733  
QY 1109 CGTGTCTTACGATTCGCGGCTCCCGATTCGAGCGCATCGCTTCTATCGCTTCTTGA 1168  
DB 734 CGTGTCTTACGATTCGCGGCTCCCGATTCGAGCGCATCGCTTCTATCGCTTCTTGA 793  
QY 1169 CGAGTTCTTCTGAG 1182  
DB 794 CGAGTTCTTCTGAG 807

RESULT 7

CK298208

LOCUS

DEFINITION

CK298208 947 bp mRNA linear EST 02-AUG-2004  
EST760922 Nicotiana benthamiana mixed tissue cDNA library,  
normalized, full-length Nicotiana benthamiana cDNA clone NEMDE30 5'  
end, mRNA sequence.

ACCESSION

CK298208

VERSION

KEYWORDS

SOURCE

ORGANISM

Nicotiana benthamiana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamiales; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 947)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,  
Staskawicz, B., Jin, H. and Baker, B.

Generation of EST sequences from Nicotiana benthamiana

Unpublished (2003)

Other ESTs: EST760923

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from the University of Arizona Genomics

Institute via http://genome.arizona.edu/orders/

Seq primer: ART TAG GTG ACA CPA TAG.

Location/Qualifiers

1..947

/organism="Nicotiana benthamiana"

/mol\_type="mRNA"

/db\_xref="taxon:4100"

/clone="NEMDE30"

/tissue\_type="abiotic and biotic stress-treated leaves,

callus tissue and root tissue"

/lab\_host="DH10B-TonA"

/clone\_lib="Nicotiana benthamiana mixed tissue cDNA

library, normalized, full-length"

/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;

supplier: RNA was isolated from Nicotiana benthamiana

tissues that include callus, roots from liquid culture

grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),

cold-stressed leaves (5 C 3 hr, 6hr), and pathogen

challenged leaves (Pseudomonas syringae pv tomato 12 hr;

FEATURES

source

```

end, mRNA sequence.
CK283361
VERSION CK283361.1 GI:39855898
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE asterids; lamids; Solanales; Solanaceae; Nicotiana.
JOURNAL 1 (bases 1 to 954)
COMMENT Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Skaskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Other ESTs: EST746084
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES
Location/Qualifiers
source
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/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
amounts."
ORIGIN
Query Match
Best Local Similarity 9.9%; Score 794; DB 7; Length 954;
Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 389 GATTGAACAGATGGATTGCGACGAGTTCTCCGGCGCTTGGTGAGAGGCTATTCCG 448
DB 14 GATTGAACAGATGGATTGCGACGAGTTCTCCGGCGCTTGGTGAGAGGCTATTCCG 73
QY 449 CTATGACTGGGCACACAGACATCGGCTCTGATGCGCGCTTCCGGTTCAGC 508
DB 74 CTATGACTGGGCACACAGACATCGGCTCTGATGCGCGCTTCCGGTTCAGC 133
QY 509 GCAGGGGCGCGGTTCTTTTGTCAAGACCGACCTGTCCGGTCCCTGAATGAATGCA 568
DB 134 GCAGGGGCGCGGTTCTTTTGTCAAGACCGACCTGTCCGGTCCCTGAATGAATGCA 193
QY 569 GGACGAGGCGCGGCTATCGTGGCTGCGCAGCGGCTTCTTGGCAGCTGTGCT 628
DB 194 GGACGAGGCGCGGCTATCGTGGCTGCGCAGCGGCTTCTTGGCAGCTGTGCT 253
QY 629 CGACGTTGTCACTGAAGCGGAGGAGTCTGCTGCTATTGGCGGAAGTCCGGGCGAGA 688
DB 254 CGACGTTGTCACTGAAGCGGAGGAGTCTGCTGCTATTGGCGGAAGTCCGGGCGAGA 313
QY 689 TCTCTGTGATCTCACTTGTCTTCTGCGGAGAAAGTATCCATCATGCTGATGCAATGG 748
DB 314 TCTCTGTGATCTCACTTGTCTTCTGCGGAGAAAGTATCCATCATGCTGATGCAATGG 373

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QY 749 GCGGCTGCATACCGCTTGATCCGCTACTGCGCATTCGACCAACGCGAAACATCGCAT 808
DB 374 GCGGCTGCATACCGCTTGATCCGCTACTGCGCATTCGACCAACGCGAAACATCGCAT 433
QY 809 CGAGCGAGCAGCTACTCGGATCGGATGGAAGCCGGTCTTGTGATCAGGATGATCTGACGAAGA 868
DB 434 CGAGCGAGCAGCTACTCGGATCGGATGGAAGCCGGTCTTGTGATCAGGATGATCTGACGAAGA 493
QY 869 GCATCAGGGGCTGCGCGCAGCCGAACTGTTGCGCAGGCTCAAGCGCGGATGCGCGGCG 928
DB 494 GCATCAGGGGCTGCGCGCAGCCGAACTGTTGCGCAGGCTCAAGCGCGGATGCGCGGCG 553
QY 929 CGAGGATCTCGTCTGATGACCCATGCGGATGCGCTTGTCCGGAATATCATCGTGAAATGG 988
DB 554 CGAGGATCTCGTCTGATGACCCATGCGGATGCGCTTGTCCGGAATATCATCGTGAAATGG 613
QY 989 CCGCTTTTCTGATCATCGACTGTGGCGGCTGGTGTGGCGGACCGCTATCAGGACAT 1048
DB 614 CCGCTTTTCTGATCATCGACTGTGGCGGCTGGTGTGGCGGACCGCTATCAGGACAT 673
QY 1049 AGCGTTGGCTACCCGCTGATATTGCTGAAGAGCTTGGCGCGAATGGGCTGACCGCTTCT 1108
DB 674 AGCGTTGGCTACCCGCTGATATTGCTGAAGAGCTTGGCGCGAATGGGCTGACCGCTTCT 733
QY 1109 CGTCTTTTACGGTATCGCGCTCCGATTCGCGAGCGCATCGCTTCTATCGCTTCTTGA 1168
DB 734 CGTCTTTTACGGTATCGCGCTCCGATTCGCGAGCGCATCGCTTCTATCGCTTCTTGA 793
QY 1169 CGAGTTCTTCTGAG 1182
DB 794 CGAGTTCTTCTGAG 807

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RESULT 9
LOCUS CK288185
DEFINITION EST750907 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NEMBE61 5',
end, mRNA sequence.
ACCESSION CK288185
VERSION CK288185.1
KEYWORDS GI:39865462
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE asterids; lamids; Solanales; Solanaceae; Nicotiana.
JOURNAL 1 (bases 1 to 811)
COMMENT Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Skaskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES
Location/Qualifiers
source
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/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
amounts."

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tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN		Query Match	9.7%;	Score 778.8;	DB 7;	Length 811;
		Best Local Similarity	99.7%;	Pred. No. 3.3e-170;		
		Matches 780;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	386	CATGATTGCAACAAAGATGATGACGACGAGTTCTCCGGCGCTTGGGTGGAGAGCTATT	445			
DB	30	CATGATTGACACAGATGATGATGACGACGAGTTCTCCGGCGCTTGGGTGGAGAGCTATT	89			
QY	446	CGGCTATGACTGGGCAACACAGCAATCGCTGCTCTGATGCGCGCTGTCGGCTGTC	505			
DB	90	CGGCTATGACTGGGCAACACAGCAATCGCTGCTCTGATGCGCGCTGTCGGCTGTC	149			
QY	506	AGCGAGGGGCGCGCTTCTTTTGTCAAGACCGACCTGTCCGGTGCCTGAAATGAAT	565			
DB	150	AGCGAGGGGCGCGCTTCTTTTGTCAAGACCGACCTGTCCGGTGCCTGAAATGAAT	209			
QY	566	CGAGACGAGGACGCGCTATCGTGGCTGGCCAGCAGCGGCTTCTTGGCGACTGT	625			
DB	210	CGAGACGAGGACGCGCTATCGTGGCTGGCCAGCAGCGGCTTCTTGGCGACTGT	269			
QY	626	GCTCGAGCTTGTCACTGAAGCGGGAAGGACTGGCTGCTATTGGGCGAAGTGCCGGGCA	685			
DB	270	GCTCGAGCTTGTCACTGAAGCGGGAAGGACTGGCTGCTATTGGGCGAAGTGCCGGGCA	329			
QY	686	GGATCTCTGTATCTCACTGCTCTGCGGAGAAAGTATCCATCATGCTGCTGATGCAAT	745			
DB	330	GGATCTCTGTATCTCACTGCTCTGCGGAGAAAGTATCCATCATGCTGCTGATGCAAT	389			
QY	746	CGCGCGCTGCATACGCTTGCATCGGCTACCTGCCATTCGACCAACGGAACATCG	805			
DB	390	CGCGCGCTGCATACGCTTGCATCGGCTACCTGCCATTCGACCAACGGAACATCG	449			
QY	806	CATCGAGCGAGCGATCTCGATGGAAGCGGCTTGTGATCAGATGATCTGGACGA	865			
DB	450	CATCGAGCGAGCGATCTCGATGGAAGCGGCTTGTGATCAGATGATCTGGACGA	509			
QY	866	AGAGCATCAGGGCTCGCGCCAGCCGAACTGTTCCGCGAGGCTCAAGCGCGCATGCCGA	925			
DB	510	AGAGCATCAGGGCTCGCGCCAGCCGAACTGTTCCGCGAGGCTCAAGCGCGCATGCCGA	569			
QY	926	CGGCGAGGATCTCGTCTGTGACCCATGGCGATGCTGCTTGGCGGAATATCATGGTGGAAA	985			
DB	570	CGGCGAGGATCTCGTCTGTGACCCATGGCGATGCTGCTTGGCGGAATATCATGGTGGAAA	629			
QY	986	TGGCGGCTTTTCTGGAATTCATGACTGTGGCGGCTGGTGTGGCGGCGGATGCGGCTT	1045			
DB	630	TGGCGGCTTTTCTGGAATTCATGACTGTGGCGGCTGGTGTGGCGGCGGATGCGGCTT	589			
QY	1046	CATAGCGTTGCTACCCGCTGATATGCTGAAGAGCTTGGCGGCGGAAATGGGCTGACCGCTT	1105			
DB	690	CATAGCGTTGCTACCCGCTGATATGCTGAAGAGCTTGGCGGCGGAAATGGGCTGACCGCTT	749			
QY	1106	CCTCGTGTCTTACGGTATCGCGCTCCCGATTCGAGCGCATCGGCTTCTATCGGCTTCT	1165			
DB	750	CCTCGTGTCTTACGGTATCGCGCTCCCGATTCGAGCGCATCGGCTTCTATCGGCTTCT	809			
QY	1166	TG 1167				
DB	810	TG 811				

CK288711 878 bp mRNA linear EST 02-AUG-2004  
LOCUS EST751433 Nicotiana benthamiana mixed tissue cDNA library,  
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NEMBI49 5'  
end, mRNA sequence.  
CK288711 GI:39866496  
EST.  
Nicotiana benthamiana  
ORGANISM Nicotiana benthamiana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (Bases 1 to 878)  
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,  
Staskawicz, B., Jin, H. and Baker, B.  
Generation of EST sequences from Nicotiana benthamiana  
Unpublished (2003)  
Contact: Robin Buell  
The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potato-array@tigr.org  
Clones can be requested from the University of Arizona Genomics  
Institute via http://genome.arizona.edu/orders/  
Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers  
1..878  
/organism="Nicotiana benthamiana"  
/mol\_type="mRNA"  
/db\_xref="taxon:4100"  
/clone="NEMBI49"  
/tissue\_type="abiotic and biotic stress-treated leaves,  
callus tissue and root tissue"  
/lab\_host="DH10B-TonA"  
/clone\_lib="Nicotiana benthamiana mixed tissue cDNA  
library, normalized, full-length"  
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;  
supplier: RNA was isolated from Nicotiana benthamiana  
tissues that include callus, roots from liquid culture  
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),  
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen  
challenged leaves (Pseudomonas syringae pv tomato 12 hr;  
Xanthomonas campestris pv campestris 12 hr, 18hr;  
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas  
campestris pv vesicatoria 18hr). RNA was isolated from  
these tissues and pooled in approximately equal molar  
amounts."

ORIGIN		Query Match	7.3%;	Score 587;	DB 7;	Length 878;
		Best Local Similarity	100.0%;	Pred. No. 9.3e-126;		
		Matches 587;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	596	GGCCACGACGCGGCTTCTTTCGCGAGCTGTCTCGACGTTCTCATGAGCGGGAAGGGA	655			
DB	1	GGCCACGACGCGGCTTCTTTCGCGAGCTGTCTCGACGTTCTCATGAGCGGGAAGGGA	60			
QY	656	CTGGCTGTATTTGGCGAAGTGGCGGCGAGATCTCTGTCTCATCTACCTTGTCTCTGC	715			
DB	61	CTGGCTGTATTTGGCGAAGTGGCGGCGAGATCTCTGTCTCATCTACCTTGTCTCTGC	120			
QY	716	CGAGAAAGTATCCATGCTGCTGATGCAATCGGCGGCTGCATACGCTTGTATCGGCTAC	775			
DB	121	CGAGAAAGTATCCATGCTGCTGATGCAATCGGCGGCTGCATACGCTTGTATCGGCTAC	180			
QY	776	CTGCCCATTCGACCAACCAAGCGAAACATCGCATCGAGCGAGCAGTACTCGGATGGAAGC	835			
DB	181	CTGCCCATTCGACCAACCAAGCGAAACATCGCATCGAGCGAGCAGTACTCGGATGGAAGC	240			
QY	836	CGGTCTTGTGATCAGGATGATCTCGACGAGAGCATCAGGGGCTCGGCCAGCGAACT	895			
DB	241	CGGTCTTGTGATCAGGATGATCTCGACGAGAGCATCAGGGGCTCGGCCAGCGAACT	300			

QY 896 GTTCCAGGCTCAAGGCGCATGCGCGGCGGAGGATCTCGTGTGACCCATGGCGA 955  
 Db 301 GTTCCAGGCTCAAGGCGCGCATGCGCGGCGGAGGATCTCGTGTGACCCATGGCGA 360  
 QY 956 TGCTGTGTCGCGAATATCATGTGTGAAATGGCGCTTTTCTCGATTCATCGACTGTGG 1015  
 Db 361 TGCTGTGTCGCGAATATCATGTGTGAAATGGCGCTTTTCTCGATTCATCGACTGTGG 420  
 QY 1016 CCGGCTGGGTGTGGCGGACCGCTATCAGACATAGCGTTGGCTACCGGTGATATGGCTGA 1075  
 Db 421 CCGGCTGGGTGTGGCGGACCGCTATCAGACATAGCGTTGGCTACCGGTGATATGGCTGA 480  
 QY 1076 AGAGCTTGGCGGGAATGGGCTGACCGCTTCCCTCGTCTTACGGTATCGCGTCCCGA 1135  
 Db 481 AGAGCTTGGCGGGAATGGGCTGACCGCTTCCCTCGTCTTACGGTATCGCGTCCCGA 540  
 QY 1136 TTGCGAGCGCATCGCTTTCATCGCTTCTTGACGAGTCTTCTGAG 1182  
 Db 541 TTGCGAGCGCATCGCTTTCATCGCTTCTTGACGAGTCTTCTGAG 587

## RESULT 11

AQ361914

LOCUS

DEFINITION 789 bp DNA linear GSS 03-FEB-1999  
 clone mgxb0005K01f CUGI Rice Blast BAC Library Magnaporthe grisea genomic

ACCESSION

AQ361914

VERSION

AQ361914.1

KEYWORDS

GSS.

SOURCE

ORGANISM

Magnaporthe grisea (anamorph: Pyricularia grisea)

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

1 (bases 1 to 789)

Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,

Phillips, K., Sasinsowski, M., Wing, R.A., and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Magnaporthe grisea

Genome

Unpublished (1998)

Contact: Dean RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson University, Clemson, SC 29634

Tel: 864 656 5737

Fax: 864 656 4293

Email: rdean@clemson.edu

Seq primer: TAATACGACTCACTATAGG

Class: BAC ends

High quality sequence start: 41

High quality sequence stop: 392.

Location/Qualifiers

1..789

/organism="Magnaporthe grisea"

/mol\_type="genomic DNA"

/strain="70-15"

/db\_xref="taxon:148305"

/clone="mgxb0005K01f"

/tissue\_type="Protoplasts"

/lab\_host="E. coli DH10B"

/clone\_lib="CUGI Rice Blast BAC Library"

/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;

Rice blast is one of the most devastating fungal diseases

of rice world wide. It is a filamentous ascomycete with

a haploid genome (n=7) of approximately 40 Mbp. Rice

blast is an important model fungal pathogen for studying

numerous aspects of the fungal-host interaction. In

order to facilitate genome wide analysis, a BAC library

containing 9216 clones with an average insert size of 130

kbp was constructed. This library represents greater

than 25X genome coverage. High density colony filters

are available upon request."

ORIGIN

## Query Match

Best Local Similarity 7.2%; Score 577.4; DB 8; Length 789;

Matches 584; Conservative 97.8%; Pred. No. 1.6e-123;

Mismatches 0; Indels 0; Gaps 0;

QY 581 GCGCTATCTGCTGGCTGCCACGACGCGGCTTCTTGGCGAGCTGTGTCGACGTTGTCAC 640  
 Db 39 GCGCTATCTGCTGGCTGCCACGACGCGGCTTCTTGGCGAGCTGTGTCGACGTTGTCAC 98  
 QY 641 TGAAGCGGGAAGGAGCTGGCTGTATTGGCGAAGTGCCTGGGCGAGCATCTCTGTGTCATC 700  
 Db 99 TGAAGCGGGAAGGAGCTGGCTGTATTGGCGAAGTGCCTGGGCGAGCATCTCTGTGTCATC 158  
 QY 701 TCACCTTGTCTTCCGCGAGAAATATCCATCATGGCTGATGCAATGGCGGCTGTCATAC 760  
 Db 159 TCACCTTGTCTTCCGCGAGAAATATCCATCATGGCTGATGCAATGGCGGCTGTCATAC 218  
 QY 761 GCTTGATCGGCTTACCTGCCATTCGACCAACCAAGCGAAATCGCATCGAGGAGCAGC 820  
 Db 219 GCTTGATCGGCTTACCTGCCATTCGACCAACCAAGCGAAATCGCATCGAGGAGCAGC 278  
 QY 821 TACTCGATGGAAGCGGCTTGTTCGATCAGGATGATCTGGACGAGAGCATCAGGGGCT 880  
 Db 279 TACTCGATGGAAGCGGCTTGTTCGATCAGGATGATCTGGACGAGAGCATCAGGGGCT 338  
 QY 881 CCGCGCAGCGCAACTGTTGCCAGGCTCAAGCGGCGCATGCCCGACGCGGAGATCTCGT 940  
 Db 339 CCGCGCAGCGCAACTGTTGCCAGGCTCAAGCGGCGCATGCCCGACGCGGAGATCTCGT 398  
 QY 941 CQTGACCCATGCGGATGCTGCTCCGAAATATCATGTGGAATGCGCGCTTTCTG 1000  
 Db 399 CQTGACCCATGCGGATGCTGCTCCGAAATATCATGTGGAATGCGCGCTTTCTG 458  
 QY 1001 ATTCATCGACTGTGCGCGCTGGGTGTGGCGACCGCTATCAGGACATAGGTTGGCTAC 1060  
 Db 459 ATTCATCGACTGTGCGCGCTGGGTGTGGCGACCGCTATCAGGACATAGGTTGGCTAC 518  
 QY 1061 CCGTGATATTCCTGAAGAGCTTGGCGGAAATGGGCTTGACCGCTTCTTCGCTTTACGG 1120  
 Db 519 CCGTGATATTCCTGAAGAGCTTGGCGGAAATGGGCTTGACCGCTTCTTCGCTTTACGG 578  
 QY 1121 TATCGCGCTCCCGATTTCGAGCGATCGCTTCTATCGCTTCTTCGCGAGTTCTT 1177  
 Db 579 TATCGCGCTCCCGATTTCGAGCGATCGCTTCTATCGCTTCTTCGCGAGTTCTT 635

## RESULT 12

AQ398387

LOCUS

DEFINITION

620 bp DNA linear GSS 06-MAR-1999  
 clone mgxb0009J05f CUGI Rice Blast BAC Library Magnaporthe grisea genomic

ACCESSION

AQ398387

VERSION

AQ398387.1

KEYWORDS

GSS.

SOURCE

ORGANISM

Magnaporthe grisea (anamorph: Pyricularia grisea)

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

1 (bases 1 to 620)

Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,

Phillips, K., Sasinsowski, M., Wing, R.A., and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Magnaporthe grisea

Genome

Unpublished (1998)

Contact: Dean RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson University, Clemson, SC 29634

Tel: 864 656 5737

Fax: 864 656 4293

Email: rdean@clemson.edu

Seq primer: TAATACGACTCACTATAGG

Class: BAC ends

High quality sequence stop: 187.

## FEATURES

source

FEATURES  
source  
1. .620  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="70-15"  
/db\_xref="taxon:148305"  
/clones="mgxb000905f"  
/tissue\_type="Protoplasts"  
/lab\_host="E. coli DH10B"  
/clone\_lib="CUGI Rice Blast BAC Library"  
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;  
Rice blast is one of the most devastating fungal diseases  
of rice world wide. It is a filamentous ascomycete with  
a haploid genome (n=7) of approximately 40 Mbp. Rice  
blast is an important model fungal pathogen for studying  
numerous aspects of the fungal-host interaction. In  
order to facilitate genome wide analysis, a BAC library  
containing 9216 clones with an average insert size of 130  
kbp was constructed. This library represents greater  
than 25X genome coverage. High density colony filters  
are available upon request."

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1. .549  
Location/Qualifiers  
/organism="Schedonorus arundinaceus"  
/mol\_type="mRNA"  
/cultivar="PI283316"  
/db\_xref="taxon:4606"  
/clone="NF32c08f44"  
/tissue\_type="shoot"  
/lab\_host="E. coli"  
/clone\_lib="Tall Fescue PI283316 44 deg C Heat Stress SSH  
cDNA"  
/note="Vector: PCR 2.1-TOPO; Site 1: EcoR I; Site 2: EcoR  
I; BD/Clontech PCR-select cDNA subtraction library"

Query Match  
Best Local Similarity 98.8%; Pred. No. 2e-115;  
Matches 543; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

556 TGAATGAACATGACGAGCAGCGGCTATCGTGGCTGGCCACGCGGCTCTT 615  
6 TGAATGAACATGACGAGCAGCGGCTATCGTGGCTGGCCACGCGGCTCTT 65  
616 GCGCAGCTGTCTCGACGTTGTCTCACTGAAGCGGAAGGAGTGGCTGCTATTGGCGGAAG 675  
66 GCGCAGCTGTCTCGACGTTGTCTCACTGAAGCGGAAGGAGTGGCTGCTATTGGCGGAAG 125  
676 TGCCGGGCGAGGATCTCTGTCTCATCTCACCTTGTCTTCCGCGAGAAAGTATCATCATGG 735  
126 TGCCGGGCGAGGATCTCTGTCTCATCTCACCTTGTCTTCCGCGAGAAAGTATCATCATGG 185  
736 CTGATGCAATCGCGGCTGTGATAGCTTGTATCGGCTACCTGCGCCATTCGACCAACCAAG 795  
186 CTGATGCAATCGCGGCTGTGATAGCTTGTATCGGCTACCTGCGCCATTCGACCAACCAAG 245  
796 CGAAACATCGGATCGAGGAGCAGCCTATCTCGATGGAAGCGGCTTGTGATCAGGATG 855  
246 CGAAACATCGGATCGAGGAGCAGCCTATCTCGATGGAAGCGGCTTGTGATCAGGATG 305  
856 ATCTGGACGAAGAGCATCAGGGGCTCGCGCAGCGAACTGTTCGACGCTCAGGCGC 915  
306 ATCTGGACGAAGAGCATCAGGGGCTCGCGCAGCGAACTGTTCGACGCTCAGGCGC 365  
916 GATGCGCGAGCGGAGGATCTCGTCTGACCCATCGCGATGCTCTTGGCCGAATATCA 975  
366 GATGCGCGAGCGGAGGATCTCGTCTGACCCATCGCGATGCTCTTGGCCGAATATCA 425  
976 TGGTGGAATATGCGCGCTTTTCTTGATTCATCTGACTGTGCGCGCTGGGTGTGGCGAC 1035

Query Match  
Best Local Similarity 98.8%; Pred. No. 2e-115;  
Matches 543; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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126 TGCCGGGCGAGGATCTCTGTCTCATCTCACCTTGTCTTCCGCGAGAAAGTATCATCATGG 185  
736 CTGATGCAATCGCGGCTGTGATAGCTTGTATCGGCTACCTGCGCCATTCGACCAACCAAG 795  
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796 CGAAACATCGGATCGAGGAGCAGCCTATCTCGATGGAAGCGGCTTGTGATCAGGATG 855  
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306 ATCTGGACGAAGAGCATCAGGGGCTCGCGCAGCGAACTGTTCGACGCTCAGGCGC 365  
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Query Match  
Best Local Similarity 98.8%; Pred. No. 2e-115;  
Matches 543; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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616 GCGCAGCTGTCTCGACGTTGTCTCACTGAAGCGGAAGGAGTGGCTGCTATTGGCGGAAG 675  
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186 CTGATGCAATCGCGGCTGTGATAGCTTGTATCGGCTACCTGCGCCATTCGACCAACCAAG 245  
796 CGAAACATCGGATCGAGGAGCAGCCTATCTCGATGGAAGCGGCTTGTGATCAGGATG 855  
246 CGAAACATCGGATCGAGGAGCAGCCTATCTCGATGGAAGCGGCTTGTGATCAGGATG 305  
856 ATCTGGACGAAGAGCATCAGGGGCTCGCGCAGCGAACTGTTCGACGCTCAGGCGC 915  
306 ATCTGGACGAAGAGCATCAGGGGCTCGCGCAGCGAACTGTTCGACGCTCAGGCGC 365  
916 GATGCGCGAGCGGAGGATCTCGTCTGACCCATCGCGATGCTCTTGGCCGAATATCA 975  
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916 GATGCGCGAGCGGAGGATCTCGTCTGACCCATCGCGATGCTCTTGGCCGAATATCA 975  
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Query Match  
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/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;  
Rice blast is one of the most devastating fungal diseases  
of rice world wide. It is a filamentous ascomycete with  
a haploid genome (n=7) of approximately 40 Mbp. Rice  
blast is an important model fungal pathogen for studying  
numerous aspects of the fungal-host interaction. In  
order to facilitate genome wide analysis, a BAC library  
containing 9216 clones with an average insert size of 130  
kbp was constructed. This library represents greater  
than 25X genome coverage. High density colony filters  
are available upon request."

Query Match  
Best Local Similarity 98.8%; Pred. No. 2e-119; 7; Indels 0; Gaps 0;

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1 GTTCTTGGCGAGCTGTCTGACGTTGTCACTGAAGCGGAGGAGTGGCTGCTATTG 60  
669 GCGGAAGTGGCGGAGGAGTCTCTGTCTCATCTCACCTTGTCTTCCGGAAGTATCC 728  
61 GCGGAAGTGGCGGAGGAGTCTCTGTCTCATCTCACCTTGTCTTCCGGAAGTATCC 120  
729 ATCATGCTGATGCAATGCGGCGGCTGATACGCTTGTATCGGCTACCTGCCATTCGAC 788  
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181 CACCAAGCAAAATCGCATCGAGCAGCAGTACTCGGATGGAAGCGGCTTGTGCGAT 240  
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301 AAGCGCGCATGCGCGAGGATCTCTGCTGACCCATGCGATGCGCTTGGCGG 360  
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421 GCGGACCCCTATCAGGACATAGCTTGGTACCCGCTGATATGCTGGAAGCTTGGCGG 480  
1089 GAATGGGCTGACCGCTTCTGCTGCTTTACGCTATCGGCTCCGATTCGAGCGGCATC 1148  
481 GAATGGGCTGACCGCTTCTGCTGCTTTACGCTATCGGCTCCGATTCGAGCGGCAT 540  
1149 GCCTTCTATGCTTCTTACGAGGTTCTTCT 1179  
541 GCCTTCTATGCTTCTTACGAGGTTCTTCT 571

Query Match  
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609 GTTCTTGGCGAGCTGTCTGACGTTGTCACTGAAGCGGAGGAGTGGCTGCTATTG 668  
1 GTTCTTGGCGAGCTGTCTGACGTTGTCACTGAAGCGGAGGAGTGGCTGCTATTG 60  
669 GCGGAAGTGGCGGAGGAGTCTCTGTCTCATCTCACCTTGTCTTCCGGAAGTATCC 728  
61 GCGGAAGTGGCGGAGGAGTCTCTGTCTCATCTCACCTTGTCTTCCGGAAGTATCC 120  
729 ATCATGCTGATGCAATGCGGCGGCTGATACGCTTGTATCGGCTACCTGCCATTCGAC 788  
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789 CACCAAGCAAAATCGCATCGAGCAGCAGTACTCGGATGGAAGCGGCTTGTGCGAT 848  
181 CACCAAGCAAAATCGCATCGAGCAGCAGTACTCGGATGGAAGCGGCTTGTGCGAT 240  
849 CAGGATGATCTGGAAGAGCATCAGGGGCTCGCGCAGCGCAACTGTTGCCAGGCTC 908  
241 CAGGATGATCTGGAAGAGCATCAGGGGCTCGCGCAGCGCAACTGTTGCCAGGCTC 300  
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969 AATATCATGTTGGAATATGCGGCTTTCTGGAATTCATCGACTGTGCGCGCTGGGTG 1028  
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1089 GAATGGGCTGACCGCTTCTGCTGCTTTACGCTATCGGCTCCGATTCGAGCGGCATC 1148  
481 GAATGGGCTGACCGCTTCTGCTGCTTTACGCTATCGGCTCCGATTCGAGCGGCAT 540  
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61 GCGGAAGTGGCGGAGGAGTCTCTGTCTCATCTCACCTTGTCTTCCGGAAGTATCC 120  
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241 CAGGATGATCTGGAAGAGCATCAGGGGCTCGCGCAGCGCAACTGTTGCCAGGCTC 300  
909 AAGCGCGCATGCGCGAGGATCTCTGCTGACCCATGCGATGCGCTTGGCGG 968  
301 AAGCGCGCATGCGCGAGGATCTCTGCTGACCCATGCGATGCGCTTGGCGG 360  
969 AATATCATGTTGGAATATGCGGCTTTCTGGAATTCATCGACTGTGCGCGCTGGGTG 1028  
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541 GCCTTCTATGCTTCTTACGAGGTTCTTCT 571

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NF32c08f44.r1 Tall Fescue PI283316 44 deg C Heat Stress SSH cDNA  
DEFINITION  
Schedonorus arundinaceus cDNA clone NF32c08f44 5', mRNA sequence.

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VERSION     AQ447874.1 GI:4577011
KEYWORDS    GSS.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM    Magnaporthe grisea
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            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
            1 (bases 1 to 561)
AUTHORS     Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
            Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
TITLE       A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
            Genome
JOURNAL     Unpublished (1998)
COMMENT     Contact: Dean RA
            Clemson University Genomics Institute
            100 Jordan Hall, Clemson University, Clemson, SC 29634
            Tel: 864 656 5737
            Fax: 864 656 4293
            Email: rdean@clemson.edu
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                    /notes="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
                    Rice blast is one of the most devastating fungal diseases
                    of rice world wide. It is a filamentous ascomycete with
                    a haploid genome (n=7) of approximately 40 Mbp. Rice
                    blast is an important model fungal pathogen for studying
                    numerous aspects of the fungal-host interaction. In
                    order to facilitate genome wide analysis, a BAC library
                    containing 9216 clones with an average insert size of 130
                    kbp was constructed. This library represents greater
                    than 25X genome coverage. High density colony filters
                    are available upon request."

ORIGIN
Query Match 6.4%; Score 514.8; DB 8; Length 561;
Best Local Similarity 99.6%; Pred. No. 6.4e-109;
Matches 516; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      104  GACGAGCAGCGCGGTATCGTGGCTGGCCACGACGCGCGTTCCTTGGCAGCTGTGCTC 163
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QY      870  CATCAGGGGCTCGCGCCAGCCGAACTGTTGCGCAGGCTCAAGGCGCGCATGCCGACGCG 929
Db      404  CATCAGGGGCTCGCGCCAGCCGAACTGTTGCGCAGGCTCAAGGCGCGCATGCCGACGCG 463
QY      930  GAGGATCTCGTCGTCACCCATGCGCATGCGCTCTTGGCGAATATCATGTTGGAATGCG 989
Db      464  GAGGATCTCGTCGTCACCCATGCGCATGCGCTCTTGGCGAATATCATGTTGGAATGCG 523
QY      990  CGCTTTCTGGATTCATCGACTGTGCGCGCTGGGTGT 1027
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RESULT 15
LOCUS   AQ447775
DEFINITION   mgxb0011E13f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
              clone mgxb0011E13f, genomic survey sequence.
ACCESSION   AQ447775
VERSION     AQ447775.1 GI:4576912
KEYWORDS    GSS.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM    Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
            1 (bases 1 to 509)
AUTHORS     Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
            Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
TITLE       A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
            Genome
JOURNAL     Unpublished (1998)
COMMENT     Contact: Dean RA
            Clemson University Genomics Institute
            100 Jordan Hall, Clemson University, Clemson, SC 29634
            Tel: 864 656 5737
            Fax: 864 656 4293
            Email: rdean@clemson.edu
            Seq primer: TAATACGACTCACTATAGGG
            Class: BAC ends
            High quality sequence stop: 342.
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                    /lab_host="E. coli DH10B"
                    /clone_lib="CUGI Rice Blast BAC Library"
                    /notes="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
                    Rice blast is one of the most devastating fungal diseases
                    of rice world wide. It is a filamentous ascomycete with
                    of rice world wide. It is a filamentous ascomycete with

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Wed Nov 10 09:31:03 2004

a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."

ORIGIN

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Query Match          6.4%; Score 508; DB 8; Length 509;
Best Local Similarity 100.0%; Pred. No. 2.4e-107;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CGACGTTGTCACTGAAGCGGGAAGGACTGGCTGCTATTGGCGGAAGTCCCGGGCAGGA 60

Qy 689 TCTCCTGTTCATCTCACTTGTCTCTCCGAGAAAGTATCCATCATGGCTGATGCAATGCG 748
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Search completed: November 9, 2004, 10:49:37  
Job time : 14590 secs



1 PAGES: 110-113  
1 DATE: 1999-07-02  
US-09-539-601-10

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Db 6421 GTCCACACAGAGAGGGGGCGCAGCGAGCTGCTTATCGTATTTCCAGATTTGGGG 6480

Db 6421 GTCCAAACAGAGAGAGGGGGCCGCAAGCCAGCTCGCTTATCGTATTCCAGATTGGG 6480  
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Db 6481 GTTCGTGTGCGAGAGAAATGGCCCTTTAGCATGTGTTCTCCACCTCCCTCAGGGCCG 6540  
Qy 6541 ATGGGCTCTTCATACGGATTCCAAATCTCTCTGAGACAGCGGTCAGATTCTGTGTAAT 6600  
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Db 6781 ACTAATTTAAAGGGAGAACTGCGGCTATCGCGGTGCGCGAGCGGTGACTGACG 6840  
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Db 6901 AAGCTCCAGGACTGACGATGCTGCTGATGCGAGACGACCTTGTCTGTTATCTGTAAAGC 6960  
Qy 6961 GCGGGACCCAGAGAGACAGGCGAGCTTACGGGCTTCACGAGGCTATGACTAGATAC 7020  
Db 6961 GCGGGACCCAGAGAGACAGGCGAGCTTACGGGCTTCACGAGGCTATGACTAGATAC 7020  
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Db 7021 TCTGCCCCCTGGGACCCGCCCAACAGATACGACTTGGAGTTGATACATCATCG 7080  
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Db 7081 TCTCCATGTTGCTAGTTCGCGACGATGATCTGGCAAAAGGCTGACTATCTCACCCGT 7140  
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Db 7141 GACCCACACCCCTTGGCGGGCTGCTGGGAGACAGCTAGACACTCCAGTCAAT 7200  
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## RESULT 2

US-09-539-601-7

; Sequence 7, Application US/09539601C

; Patent No. 6630343

; GENERAL INFORMATION:

; APPLICANT: Bartschlag, Ralf FW

; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System

; FILE REFERENCE: all sequences

; CURRENT APPLICATION NUMBER: US/09/539,601C

; EARLIER FILING DATE: 2001-08-30

; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY

; EARLIER FILING DATE: 1999-04-03

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 8001

; TYPE: DNA

; ORGANISM: Hepatitis C virus

; FEATURE:

; NAME/KEY: 5'UTR

; LOCATION: (1)..(341)

; OTHER INFORMATION: construct I389/NS3-3'/wt

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (342)..(1193)

; OTHER INFORMATION: hepatitis C virus core-neomycin

; OTHER INFORMATION: phosphotransferase fusion protein

; FEATURE:

; NAME/KEY: RBS

; LOCATION: (1202)..(1812)

; OTHER INFORMATION: internal ribosome entry site from

; OTHER INFORMATION: encephalomyocarditis virus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1813)..(7770)

; OTHER INFORMATION: hepatitis C virus nonstructural proteins NS3-5B

; FEATURE:

; NAME/KEY: 3'UTR

; LOCATION: (7771)..(8001)

; PUBLICATION INFORMATION:
; AUTHORS: Lohmann, Volker
; AUTHORS: Kner, Frank
; AUTHORS: Koch, Jan-Oliver
; AUTHORS: Herlihan, Ulrike
; AUTHORS: Theilmann, Lorenz
; AUTHORS: Bartenschlager, Ralf
; TITLE: Replication of subgenomic hepatitis c virus RNAs in a
; TITLE: hepatoma cell line
; JOURNAL: Science
; VOLUME: 285
; PAGES: 110-113
; DATE: 1999-07-02
; US-09-539-601-7

Query Match 99.7%; Score 7967; DB 4; Length 8001;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 7989; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

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Qy	61	TCCTCAGCAGAAAGCGTCTAGCCATGCGCTTAGTATGATGATGTCGTGCGAGCTCAGGAC	120
Db	61	TCCTCAGCAGAAAGCGTCTAGCCATGCGCTTAGTATGATGATGTCGTGCGAGCTCAGGAC	120
Qy	121	CCCCCTCCCGGAGAGCCATAGTGGTCTGGGACCGGTGAGTACACCGGAATGGCAG	180
Db	121	CCCCCTCCCGGAGAGCCATAGTGGTCTGGGACCGGTGAGTACACCGGAATGGCAG	180
Qy	181	GACGACCGGGTCCCTTCTTGATCAACCCCGCTCAATGCTCGAGATTGGCGTGGCCCC	240
Db	181	GACGACCGGGTCCCTTCTTGATCAACCCCGCTCAATGCTCGAGATTGGCGTGGCCCC	240
Qy	241	GCGAGACTGCTAGCGAGTAGTGTGGTTCGCGAAGCGCTTGGTACTGCTGATAGG	300
Db	241	GCGAGACTGCTAGCGAGTAGTGTGGTTCGCGAAGCGCTTGGTACTGCTGATAGG	300
Qy	301	GTGCTTGGAGTGCCTGGGAGGTCTCGTAGCCGTGACCACTGAGCAGCAATCCTAAG	360
Db	301	GTGCTTGGAGTGCCTGGGAGGTCTCGTAGCCGTGACCACTGAGCAGCAATCCTAAG	360
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Db	361	CTCAAGAAAAACAAA-----GGGCGCGCCATGATTGAAACAAGATGATTC	420
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Db	421	ACGAGGTTCTCGGCGCGTGGGTGAGAGGCTATTGCGGTATGACTGGGCAACAAGA	480
Qy	469	CAATCGGTCTCTGATGCCCGGTGTTCCGCTGTAGCCAGCGGGCGCGCGGTCTTT	528
Db	481	CAATCGGTCTCTGATGCCCGGTGTTCCGCTGTAGCCAGCGGGCGCGCGGTCTTT	540
Qy	529	TTGTCAAGACCGACTGTGCGGTGCTGATGAACTGACGAGCAGGCGAGCGGCTAT	588
Db	541	TTGTCAAGACCGACTGTGCGGTGCTGATGAACTGACGAGCAGGCGAGCGGCTAT	600
Qy	589	CGTGGTGGCCACGACGGCGGTCTTGGCGAGCTGTCTGACGAGTGTCTGAGAGCGG	648
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Qy	649	GAAGGACTGCTGCTATTGGCGAAGTCCGGGCGAGGATCTCTGTCATCTACCTTG	708
Db	661	GAAGGACTGCTGCTATTGGCGAAGTCCGGGCGAGGATCTCTGTCATCTACCTTG	720
Qy	709	CTCTGCGCAGAAAGTATCCATCATATGCTGATGCAATCGCGGCTGATACGCTGATC	768
Db	721	CTCTGCGCAGAAAGTATCCATCATATGCTGATGCAATCGCGGCTGATACGCTGATC	780
Qy	769	CGGCTACCTGCCATTCCACCAACCGAAGACATCGATCGAGGAGCAGCTACTCGGA	828

Db	781	CGGCTACCTGCCCATTCGACCCACCAAGCGAAACATCGCATCGAGCGACAGTACTCGGA	840
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Db	841	TGGAGCGCGTCTTGTGATCAGATGATCTGGACGAGACATCAGGGGCTCGCGCAG	900
Qy	889	CCGAACTGTTTCCGCCAGGCTCAAGGCGGCGATGCCCGACGGCGAGGATCTCTGTCGACCC	948
Db	901	CCGAACTGTTTCCGCCAGGCTCAAGGCGGCGATGCCCGACGGCGAGGATCTCTGTCGACCC	960
Qy	949	ATGCGATGCTGCTTCCCGAATATCATGFGGAAAAATGGCGGCTTTTCGATTCATCG	1008
Db	961	ATGCGATGCTGCTTCCCGAATATCATGFGGAAAAATGGCGGCTTTTCGATTCATCG	1020
Qy	1009	ACTGTGCCCGCTGGGTGTGGCGACCGCTATCAGGACATAGCTTGGCTACCGGTGATA	1068
Db	1021	ACTGTGCCCGCTGGGTGTGGCGACCGCTATCAGGACATAGCTTGGCTACCGGTGATA	1080
Qy	1069	TTGCTGAAGAGCTTTGGCGGGAATGGGCTGACCGCTTCTCTGCTTTACGGTATCGCG	1128
Db	1081	TTGCTGAAGAGCTTTGGCGGGAATGGGCTGACCGCTTCTCTGCTTTACGGTATCGCG	1140
Qy	1129	CTCCGATTCGACGGGATCGCCTTCTATGCGCTTCTTGAAGGATCTTCTGAGTTAAA	1188
Db	1141	CTCCGATTCGACGGGATCGCCTTCTATGCGCTTCTTGAAGGATCTTCTGAGTTAAA	1200
Qy	1189	CAGACCAACCGGTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTCT	1248
Db	1201	CAGACCAACCGGTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTCT	1260
Qy	1249	AACGTTACTGGCCGAAAGCGCTTGGAAATAAGCGCGGTGTGGTTGCTATATGTTATTT	1308
Db	1261	AACGTTACTGGCCGAAAGCGCTTGGAAATAAGCGCGGTGTGGTTGCTATATGTTATTT	1320
Qy	1309	TCCACCATATTGCGCTTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGCTCTTCTG	1368
Db	1321	TCCACCATATTGCGCTTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGCTCTTCTG	1380
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Qy	1429	GTGAAGGAAGCAGTTCCTCTGGAAGCTTTTGAAGACAAAACAAGTCTGTGAGCGACCTT	1488
Db	1441	GTGAAGGAAGCAGTTCCTCTGGAAGCTTTTGAAGACAAAACAAGTCTGTGAGCGACCTT	1500
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Db	1501	TGCGAGCAGGAAACCCCGACCTGCGACAGGTGCTCTCGGCGCAAAAGCCAGCTGA	1560
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Qy	1609	GAAGAGTCAAAATGGCTCTCTCAAGCGTATTCAAGGGGCTGAAGGATGCCAGAG	1668
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Qy	1669	GTACCCCATTTGATGGGATCTGATCTGGGCTCGGTGCAATGCTTTTACATGTTTAG	1728
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Qy	1729	TCGAGGTTAAAAACGCTTAGGCCCCCGCAACCGGAGCGTGGTTTCTTTTGAAGAAA	1788
Db	1741	TCGAGGTTAAAAACGCTTAGGCCCCCGCAACCGGAGCGTGGTTTCTTTTGAAGAAA	1800
Qy	1789	CACGATATACCATGGGCGCTATTACGGCTTACTTCCCAACAGACGCGAGGCTTCTGCG	1848
Db	1801	CACGATATACCATGGGCGCTATTACGGCTTACTTCCCAACAGACGCGAGGCTTCTGCG	1860
Qy	1849	TGCATCATCTAGCTTACAGGCGGGAAGGAAACAGGTCGAGGGGAGGTCCAAAGTG	1908
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1909 GTCTCACCAGCAACAATCTTTCTGCGGACCTCGGTCAATGGCGTGTGTTGGAATGTC 1968  
1921 GTCTCACCAGCAACAATCTTTCTGCGGACCTCGGTCAATGGCGTGTGTTGGAATGTC 1980  
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1981 TATCATGTGTCGGGCTCAAGACCCCTTGGCGGCCCAAGGGCCCAATCAACCAATGTAC 2040  
2029 ACCAATGTGGACAGGACCTCGTTCGGCTCGCAAGCGCCCCCGGGCGCGTTCCTTGACA 2088  
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2101 CAATGCACTGTCGGCAGCTCGGACCTTTACTTTGGTCAAGGACATGCCGATGTCAATCGG 2160  
2149 GTGCGCCGCGGGGCGGACAGCAGGGGGGAGCTACTCTCCGCCAGGCGCGTTCCTTGACA 2208  
2161 GTGCGCCGCGGGGCGGACAGCAGGGGGGAGCTACTCTCCGCCAGGCGCGTTCCTTGACA 2220  
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RESULT 3  
US-09-539-601-22  
; Sequence 22, Application US/09539601C  
; Patent No. 6630343  
; GENERAL INFORMATION:  
; APPLICANT: Bartenchlagel, Ralf FW  
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System  
; FILE REFERENCE: all sequences  
; CURRENT APPLICATION NUMBER: US/09/539,601C  
; CURRENT FILING DATE: 2001-08-30  
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY  
; EARLIER FILING DATE: 1999-04-03  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 8001  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: (1)..(341)  
; OTHER INFORMATION: construct I389/NS3-3'/5.1  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (342)..(1193)  
; OTHER INFORMATION: hepatitis C virus core - neomycin  
; OTHER INFORMATION: phosphotransferase fusion protein  
; FEATURE:

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; NAME/KEY: RBS
; LOCATION: (1202)..(1812)
; OTHER INFORMATION: internal ribosome entry site from
; OTHER INFORMATION: encephalomyocarditis virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1813)..(7770)
; OTHER INFORMATION: hepatitis C virus nonstructural proteins NS3 - 5B
; OTHER INFORMATION: of cell culture-adapted clone no. 5.1
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (7771)..(8001)
; US-09-539-601-22

Query Match      99.5%; Score 7949.4; DB 4; Length 8001;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 7978; Conservative 0; Mismatches 11; Indels 12; Gaps 1;

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Db	4141	ACCAACCAACATACCTCTCTGTTTAAACATCTCTGGGGGATGGTGGCCGCCCAACTTCTCT	4200	Qy	5269	ACGGCGGAGACGGCTAAAGGTAGGCTGGCCAGGGGATCTCCCCCTCTCTTGGCCAGCTCA	5328
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Db	4201	CTTCCAGCGCT	4260	Qy	5329	TCAGCTAGCAGCTGTCTCGGCTCTCTTGAAGGCAACATGCACTACCCGTCATGACTCC	5388
Qy	4249	ATAGGCTTTGGGAAGGTCTCTGAGATATTTTGGCAGGTTATGGAGCAGGGTGGCAGGC	4308	Db	5341	TCAGCTAGCAGCTGTCTCGGCTCTCTTGAAGGCAACATGCACTACCCGTCATGACTCC	5400
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Qy	4429	CTGCGTCGGCACGTGGGCCAGGGAGGGGCTGTGCAGFTGATGAACCGGCTGTATGCG	4488	Db	5521	GAGGAGGATGAGAGGGAAGTATCCGTTCCGGCGGAGATCCTGCGAGGTCAGGAAATTC	5580
Db	4441	CTGCGTCGGCACGTGGGCCAGGGAGGGGCTGTGCAGFTGATGAACCGGCTGTATGCG	4500	Qy	5569	CCTCGAGCGATGATGGGCAACCGCCGGATTAACCCCTCCACTGTTAGAGTCTCTGG	5628
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Qy	4909	ATTAAACGCTACACACGGGCGCTGACGCGCTCTCCCGCGCCCAAAATTTCTAGGGCG	4968	Db	6001	TCCTACATGAGGACGAGCGCCCTCATCGCCATCGCTGGGAGGAAACCAAGCTGCC	6060
Db	4921	ATTAAACGCTACACACGGGCGCTGACGCGCTCTCCCGCGCCCAAAATTTCTAGGGCG	4980	Qy	6049	ATCAATGCACTGACCAACTCTTTCTCCGTCAACCAACTTGTGTCTATGTCTAACATCT	6108
Qy	4969	CTGTGGGGGTGGTGTGAGAGTACCTGAGGATGACGGGTGAGGATGAGGATGAGGATGAG	5028	Db	6061	ATCAATGCACTGACCAACTCTTTCTCCGTCAACCAACTTGTGTCTATGTCTAACATCT	6120
Db	4981	CTGTGGGGGTGGTGTGAGAGTACCTGAGGATGACGGGTGAGGATGAGGATGAGGATGAG	5040	Qy	6109	CGCAGCGCAAGCTTGGCGGACAGAAAGTCACTTTGACACTTGCAGCTTCTGAGCCAC	6168
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Db	5041	GTGACGGCATGACCACTGACACGTAAGTGGCCGCTGTAGGTTCCGGGCGCCGAAATTC	5100	Qy	6169	CACCTACCGGAGCTGTCAAGGAGATGAAGGAGGAGGCTCCACAGTTTAAGGCTAACTT	6228
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Qy	5149	CGGAGGAGGATCAATCTCTGTGCGGCTCAATCAATACCTGGTTGGTTCAGAGCTCCCA	5208	Db	6241	CTATCCGTGGAGGAGCTGTAAAGTGAAGCCGCCCACTTGGCCAGATCTAAATTTGGC	6300
Db	5161	CGGAGGAGGATCAATCTCTGTGCGGCTCAATCAATACCTGGTTGGGTTCAGAGCTCCCA	5220				

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QY	6349	TGGAAGGACCTTGCTGGGAAGACACTGAGACACCAATTGACACCAATCATGGGCAAAAAT	6408
DB	6361	TGGAAGGACCTTGCTGGGAAGACACTGAGACACCAATTGACACCAATCATGGGCAAAAAT	6420
QY	6409	GAGGTTTTCTGCGTCCAAACAGAGAAGGGGGCGCGCAAGCGCTCGCTTTATCGTATTC	6468
DB	6421	GAGGTTTTCTGCGTCCAAACAGAGAAGGGGGCGCGCAAGCGCTCGCTTTATCGTATTC	6480
QY	6469	CCAGATTTGGGGTTTCTGTGTGCGAGAAATATGGCCCTTTACGATGTGTTTCCACCCTC	6528
DB	6481	CCAGATTTGGGGTTTCTGTGTGCGAGAAATATGGCCCTTTACGATGTGTTTCCACCCTC	6540
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QY	6649	TGTTTTGACTCAACGGTGCACTGAGAAATGACATCCGTTGAGGAGTCAATCTACCAATGT	6708
DB	6661	TGTTTTGACTCAACGGTGCACTGAGAAATGACATCCGTTGAGGAGTCAATCTACCAATGT	6720
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DB	7021	ATGACTAGATACTCTGCCCCCTCTGGGACCCGCCCAAAACAGAATACGACTTGGAGTTG	7080
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RESULT 4
US-09-539-601-16
; Sequence 16, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 8001
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct I389/NS3-3'/9-13F
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1193)
; OTHER INFORMATION: hepatitis C virus core-neomycin phosph
; OTHER INFORMATION: fusion protein
; NAME/KEY: RBS

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Query Match	99.4%	Score 7947.8	DB 4	Length 8001
Best Local Similarity	99.7%	Pred. No. 0		
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Y	61	TCCTTCACGCAGAAACGCTTAGCCATGGCGTTAGTATGAGTGTCTGTGAGCCTCCAGGAC	120	
D	61	TCCTTCACGCAGAAACGCTTAGCCATGGCGTTAGTATGAGTGTCTGTGAGCCTCCAGGAC	120	
Y	121	CCCCCTCCCGGAGAGCCATAGTGGTCTTCGGGAACCGGTGAGTACACGGAAATGCCAG	180	
D	121	CCCCCTCCCGGAGAGCCATAGTGGTCTTCGGGAACCGGTGAGTACACGGAAATGCCAG	180	
Y	181	GACGACCGGGTCTCTTTCTTGATCAACCCCGCTCAATGCCTGGAGATTTGGGCGTCCGCC	240	
D	181	GACGACCGGGTCTCTTTCTTGATCAACCCCGCTCAATGCCTGGAGATTTGGGCGTCCGCC	240	
Y	241	GCAGAGCTGTAGCCGAGTAGTTGGTTCGCGAAGGCCCTTGTGGTACTGGCTGATAGG	300	
D	241	GCAGAGCTGTAGCCGAGTAGTTGGTTCGCGAAGGCCCTTGTGGTACTGGCTGATAGG	300	
Y	301	GTGCTTGGAGTGCCTCCGGGAGGTCTCTGTAGACCGTGCACCATGAGCAGAACTCTAAAC	360	
D	301	GTGCTTGGAGTGCCTCCGGGAGGTCTCTGTAGACCGTGCACCATGAGCAGAACTCTAAAC	360	
Y	361	CTCAAGAAAAACCAA-----GGGCGCGCCATGATGAAACAAGATGATTC	408	
D	361	CTCAAGAAAAACCAAAGCTTAACACCAACGGCGCGCCATGATGAAACAAGATGATTC	420	
Y	409	ACGAGGTTCTCCGGCCGTTGGGTGGAGAGCTATTGGCTATGCTGGGACACACAGA	468	
D	421	ACGAGAGTTCTCCGGCCGTTGGGTGGAGAGGCTATTGGCTATGCTGGGACACACAGA	480	
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D	481	CAATCGGCTGCTCTGATGCCCGCGTTCCTCGGCTGTACGCGAGGGGCGCCGGTCTTT	540	
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D	541	TTGTCAAGACCGACTGTGTCGGTGCCTGATGAACTGCAGACGAGGAGCGCGGCTAT	600	
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D	601	CGTGGCTGCACACGAGCGGCGTTCCTTGGCAGCTGTGCTCGACGTTGTCACTGAAGCGG	660	
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D	661	GAAGGACTGGCTGTATTGGCGAAGTCCCGGAGCGAGATCTCCTGTGATCTACCTTTG	720	
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RESULT 5  
US-09-539-601-28  
; Sequence 28, Application US/09539601C  
; Patent No. 6630343  
; GENERAL INFORMATION:  
; APPLICANT: Bartenschlager, Ralf FW  
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System  
; FILE REFERENCE: all sequences  
; CURRENT APPLICATION NUMBER: US/09/539,601C  
; CURRENT FILING DATE: 2001-08-30  
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY  
; EARLIER FILING DATE: 1999-04-03  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 8001  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: (1)..(341)  
; OTHER INFORMATION: construct I389/NS3-3'/19  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (342)..(1193)  
; OTHER INFORMATION: hepatitis C virus core - neomycin  
; OTHER INFORMATION: phosphotransferase fusion protein  
; FEATURE:  
; NAME/KEY: RBS

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; LOCATION: (1202)..(1812)
; OTHER INFORMATION: internal ribosome entry site from
; FEATURE: encephalomyocarditis virus
; NAME/KEY: CDS
; LOCATION: (1813)..(7770)
; OTHER INFORMATION: hepatitis C virus nonstructural proteins NS3 - 5B
; OTHER INFORMATION: of cell culture adapted clone no. 19
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (7771)..(8001)
US-09-539-601-28

Query Match      99.4%; Score 7941.4; DB 4; Length 8001;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 7973; Conservative 0; Mismatches 16; Indels 12; Gaps 1;

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QY	4189	CCTCCACAGCGCTCTCTGCTTCTGCTTCTGCTAGCGCGCGCATCGCTGGAGCGCTGTGGCAGC	4248	QY	5269	ACGGCGGAGACGGCTAAAGCTAGGCTGGCGAGGGATCTCCGCCCTCTCTTGGCCAGCTCA	5328
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QY	4249	ATAGCGCTTGGGAAGGTGTCTGTGGATATTTTGGAGGTATTTGGAGCGGTGGCAGGC	4308	QY	5329	TCAGCTAGCAGCTCTCTGCGCTTCTTTGAAGGCAACATGCACTACCGGTCAATCTCC	5388
DB	4261	ATAGCGCTTGGGAAGGTGTCTGTGGATATTTTGGAGGTATTTGGAGCGGTGGCAGGC	4320	DB	5341	TCAGCTAGCAGCTCTCTGCGCTTCTTTGAAGGCAACATGCACTACCGGTCAATCTCC	5400
QY	4309	GGCTCTGCGCTTAAAGTCTAGCGCGGAGATGCCCTCCACCGAGGACCTGGTTAAC	4368	QY	5389	CCGGAACGCTGACCTCATCGAGGCCAACCTCTCTGGCGGAGAGATGGCGGGACATC	5448
DB	4321	GGCTCTGCGCTTAAAGTCTAGCGCGGAGATGGCTTCCCTCCACCGAGGACCTGGTTAAC	4380	DB	5401	CCGGAACGCTGACCTCATCGAGGCCAACCTCTCTGGCGGAGAGATGGCGGGACATC	5460
QY	4369	CTACTCCCTGCTATCCTCTCCCTTGGCGCCCTAGTCTCGGGGTCTGTGGCAGCGATA	4428	QY	5449	ACCCCGTGGAGTCAAGAAATAAGTAGTAAATTTTGGACTCTTTCCAGCCGGTCCCAAGCG	5508
DB	4381	CTACTCCCTGCTATCCTCTCCCTTGGCGCCCTAGTCTCGGGGTCTGTGGCAGCGATA	4440	DB	5461	ACCCCGTGGAGTCAAGAAATAAGTAGTAAATTTTGGACTCTTTCCAGCCGGTCCCAAGCG	5520
QY	4429	CTGCGTGGCAGCTGGGGCCACAGGGAGGGGGCTGTGCAGTGTGATGAAACCGGTGTAGCG	4488	QY	5509	GAGGAGGATGAGAGGGAAGTATCCGTTCCGGCGGAGATCCTGCGGAGGTCAGGAAATTC	5568
DB	4441	CTGCGTGGCAGCTGGGGCCACAGGGAGGGGGCTGTGCAGTGTGATGAAACCGGTGTAGCG	4500	DB	5521	GAGGAGGATGAGAGGGAAGTATCCGTTCCGGCGGAGATCCTGCGGAGGTCAGGAAATTC	5580
QY	4489	TTGCGCTTGGGGGTAAACAGCTCTCCCGACGCACTATGTGCTGAGAGCGAGCTGCA	4548	QY	5569	CCTCGAGCGATGCCATATGGGCAAGCCCGGATTACAAACCTCCACTGTTAGAGTCTCG	5628
DB	4501	TTGCGCTTGGGGGTAAACAGCTCTCCCGACGCACTATGTGCTGAGAGCGAGCTGCA	4560	DB	5581	CCTCGAGCGATGCCATATGGGCAAGCCCGGATTACAAACCTCCACTGTTAGAGTCTCG	5640
QY	4549	GCAGTGTCACTCAGATCCTCTCTAGTCTTTACATCACTCAGTGTCTGAGAGGCTTCA	4608	QY	5629	AAAGGACCCGAGTACTCTCCCTCAGTGTACAGGGGTCTCATTTGGCGCTGCCAAGGCC	5688
DB	4561	GCAGGATCACTCAGATCCTCTCTAGTCTTTACATCACTCAGTGTCTGAGAGGCTTCA	4620	DB	5641	AAAGGACCCGAGTACTCTCCCTCAGTGTACAGGGGTCTCATTTGGCGCTGCCAAGGCC	5700
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QY	4669	GATTGATATGACAGGTGTTGACTGATTTCAAGACCTGGCTCCAGTCCCAAGCTCTGCCG	4728	QY	5749	TTGCTCTTGGCGAGCTCGCCACAAAGACTTTCGGCAGCTCCGAAATCTGCGGCCGTCGAC	5808
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QY	4729	CGATTCCGGGAGTCCCTTTCTCTCATGTCAAAGTGGGTACAGGGAGTCTGGCGGGC	4788	QY	5809	AGCGGACCGCAACCGCTCTCTGACCGAGCCCTCCGACGAGCGGCGAGCGGGATCCGAC	5868
DB	4741	CGATTCCGGGAGTCCCTTTCTCTCATGTCAAAGTGGGTACAGGGAGTCTGGCGGGC	4800	DB	5821	AGCGGACCGCAACCGCTCTCTGACCGAGCCCTCCGACGAGCGGCGAGCGGGATCCGAC	5880
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DB	4801	GACGGATCATGCAAAACCACTGCTCCATGTGGAAGCAGATCAACCGGACATGGAATAAC	4860	DB	5881	GTTGAGTCTGCTCTCTCATGCCCCCTTTGAGGGGAGCGCGGGGATCCGATCTCAGC	5940
QY	4849	GGTTCCATGAGGATCGTGGGCTTAGGACCTGTAGTAAACAGTGGCATGGAACATTCGCC	4908	QY	5929	GACGGTCTTGGTCTTACCGTAAGCGAGGAGGTAGTGAGGACCTGCTCTCTCTCGATG	5988
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				QY	6289	TATGGGCAAGGAGCTCGGAACTTATCAGCAAGCGCGCTTAAACCACTCCGCTCCGCTG	6348

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RESULT 6  
US-09-539-601-4  
; Sequence 4, Application US/09539601C  
; Patent No. 6630343  
; GENERAL INFORMATION:  
; APPLICANT: Bartenschlager, Ralf FW  
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System  
; FILE REFERENCE: all sequences  
; CURRENT APPLICATION NUMBER: US/09/539,601C  
; EARLIER FILING DATE: 2001-08-30  
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY  
; EARLIER FILING DATE: 1999-04-03  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 8637  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: (1)..(341)  
; OTHER INFORMATION: construct I377/NS2-3'/wt  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (342)..(1181)  
; OTHER INFORMATION: HCV core-neomycin phosphotransferase fusion  
; OTHER INFORMATION: protein  
; FEATURE:  
; NAME/KEY: RBS  
; LOCATION: (1190)..(1800)

; OTHER INFORMATION: internal ribosome entry site from  
; OTHER INFORMATION: encephalomyocarditis virus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1801)..(8406)

; OTHER INFORMATION: hepatitis C virus NS2 - 5B

; FEATURE:

; NAME/KEY: 3'UTR

; LOCATION: (8407)..(8637)

; PUBLICATION INFORMATION:

; AUTHORS: Lohmann, Volker

; AUTHORS: Krner, Frank

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Query Match 91.7%; Score 7331; DB 4; Length 8637;

Best Local Similarity 92.5%; Pred. No. 0;

Matches 7989; Conservative 0; Mismatches 0; Indels 648; Gaps 1;

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DB 1 GCCAGCCCCCGATTGGGGCGGACATCTCCACCATAGATCACTCCCTGTGAGGAACTACTG 60

QY 61 TCTTCACGACGAAAGCGTCTAGCCATGGGTTAGTATGATGTCGTCGACGCTCCAGGAC 120

DB 61 TCTTCACGACGAAAGCGTCTAGCCATGGGTTAGTATGATGTCGTCGACGCTCCAGGAC 120

QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGAACCCTGAGTACACCGGAATCCCGAG 180

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 DB 2941 ACCGAGGGTTCGAAGGGGTGACTTTGTACCGGTGAGTGTATGGAACCACTATG 3000  
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 QY 2521 GGTATATGCTTAAGGCACATGTATCGACCTTAAACATCAGAACCGGGGTAAAGCAATC 2580





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QY 6961 GCGGGGACCCAGAGGAGAGGAGGAGCTTACGCGGCTTTCACGGAGGCTATGACTAGATAC 7020
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QY 7981 AGATCAAGT 7989
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Db 8641 AGATCAAGT 8649
RESULT 8
US-10-029-907-1
; Sequence 1, Application US/10029907
; Patent No. 6706874
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; TITLE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/029,907
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 8639
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1803)...(8408)
US-10-029-907-1
Query Match 91.0%; Score 7273.8; DB 4; Length 8639;
Best Local Similarity 92.2%; Pred. No. 0;
Matches 7976; Conservative 0; Mismatches 2; Indels 671; Gaps 3;
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Db 62 TCTTACGCGAGAAAGCGTCTAGCCATGGGTTAGTATGATGTCGTCGACGCTCCAGGAC 121
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QY 241 GCGAGACTCTAGCCGAGTAGTGTGGGTGCGGAAGGCTTGTGGTACTGCTGATAGG 300
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QY 301 GTGCTTGGAGTCCCGGGGAGGTCTCGTAGACCGTGACCATGAGCAGAAATCTTAAAC 360
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QY 361 CTCAAAGAAAACCAAAAGGCGCGCATGATGAAAGATGATGACGACGAGGTTCTC 420
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Db 482 CTGATGCGCGCTGTTCCGGCTCTGACGCGAGGGGCGCGGTTCTTTTGTCAAGACCG 541
QY 541 ACCTGTCCGCTGCTGAAATGAATCTGAGGACGAGGCGCGCTATCTGCTGCGCA 600
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QY 601 CGAGCGGCTTCTTGGCGAGCTGTGCTCGACGTTGCTCACTGAAGCGGAGGAGGACTGGC 660
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Dd	602	CGACGGGGTTCCTTGGCGAGCTGTCTGCGACGTTGTCACTGAAGCGGGAAGGACTGCG	661
Qy	661	TGCTATTGGCGAAGTGGCGGCGAGGATCTCTGTCTATCTCACCTTGTCTCTGCGCGAGA	720
Dd	662	TGCTATTGGCGAAGTGGCGGCGAGGATCTCTGTCTATCTCACCTTGTCTCTGCGCGAGA	721
Qy	721	AAGTATCATCATGCTGATGCAATGGCGGCGCTCATACGCTTGATCCGGTCACTGCC	780
Dd	722	AAGTATCATCATGCTGATGCAATGGCGGCGCTCATACGCTTGATCCGGTCACTGCC	781
Qy	781	CATTGCGACCAAGCGGCAATCCATCGAGCGAGCAGTACTCGGATGGAGCCGGTC	840
Dd	782	CATTGCGACCAAGCGGCAATCCATCGAGCGAGCAGTACTCGGATGGAGCCGGTC	841
Qy	841	TGTCGATCAGGATGATCTGGACGAAGCATCAGGGCTCGCGCCAGCCGAATGTTTCG	900
Dd	842	TGTCGATCAGGATGATCTGGACGAAGCATCAGGGCTCGCGCCAGCCGAATGTTTCG	901
Qy	901	CCAGGCTCAAGCGGCGCATGCCGACGGCGAGGATCTCGTGTGACCCATGGCGATGCT	960
Dd	902	CCAGGCTCAAGCGGCGCATGCCGACGGCGAGGATCTCGTGTGACCCATGGCGATGCT	961
Qy	961	GCTTGGCCGAATATCATGCTGGAAATGSCCGCTTTCTGGATTCATCGACTGTGCGCGC	1020
Dd	962	GCTTGGCCGAATATCATGCTGGAAATGSCCGCTTTCTGGATTCATCGACTGTGCGCGC	1021
Qy	1021	TGGGTGGCGGACCGCTATCAGGACATAGCGTGGCTACCGCTGATATTCCTGAAGAGC	1080
Dd	1022	TGGGTGGCGGACCGCTATCAGGACATAGCGTGGCTACCGCTGATATTCCTGAAGAGC	1081
Qy	1081	TGGCGGCGAATGGGCTGACCGCTTCTCGTGTCTTACGGTATCGCGCTCCCGATTGCG	1140
Dd	1082	TGGCGGCGAATGGGCTGACCGCTTCTCGTGTCTTACGGTATCGCGCTCCCGATTGCG	1141
Qy	1141	AGCGCATCGCCTTATCGCCTTCTTGACGAGTCTCTGAGTT-----TAAA	1188
Dd	1142	AGCGCATCGCCTTATCGCCTTCTTGACGAGTCTCTGAGTT-----TAAA	1201
Qy	1189	CAGACCAACAGGTTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCGCT	1248
Dd	1202	CAGACCAACAGGTTTCCCTCTAGCGGATCAATTCG-----CCCGCCCGCT	1250
Qy	1249	AAGTTACTGCGGAGCGCTTGGAAATAGCGCGGTGCGTTGTATATGTTATTT	1308
Dd	1251	AAGTTACTGCGGAGCGCTTGGAAATAGCGCGGTGCGTTGTATATGTTATTT	1310
Qy	1309	TCCACCATATTGCGCTTTTGGCAATGTGAGGCGCGGAACTGCGCCTGCTTCTTG	1368
Dd	1311	TCCACCATATTGCGCTTTTGGCAATGTGAGGCGCGGAACTGCGCCTGCTTCTTG	1370
Qy	1369	ACGAGCATTCCTAGGGTCTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTC	1428
Dd	1371	ACGAGCATTCCTAGGGTCTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTC	1430
Qy	1429	GTGAGGAAGCAGTTCTCTGGAAGCTTCTTGAAGACAAACAGCTGTAGCGACCTT	1488
Dd	1431	GTGAGGAAGCAGTTCTCTGGAAGCTTCTTGAAGACAAACAGCTGTAGCGACCTT	1490
Qy	1489	TGCAGGACGCGGAACCCCGACCTGCGCAGAGTGCCTCTGCGCCAAAGGACCACTGTA	1548
Dd	1491	TGCAGGACGCGGAACCCCGACCTGCGCAGAGTGCCTCTGCGCCAAAGGACCACTGTA	1550
Qy	1549	TAAGATACCTGCAAGGGGCGCAACCCCGCTGCGCAGTGCCTGAGTTGATGTTGTG	1608
Dd	1551	TAAGATACCTGCAAGGGGCGCAACCCCGCTGCGCAGTGCCTGAGTTGATGTTGTG	1610
Qy	1609	GAAAGAGTCAATGGCTCTCTCAAGGATTCACAAAGGGGCTGGAAGGATGCCCGAAG	1668
Dd	1611	GAAAGAGTCAATGGCTCTCTCAAGGATTCACAAAGGGGCTGGAAGGATGCCCGAAG	1670
Qy	1669	GTACCCCATGATGGATCTGATCTGGGCGCTCGGTGCAATGCTTATGTTAG	1728
Dd	1671	GTACCCCATGATGGATCTGATCTGGGCGCTCGGTGCAATGCTTATGTTAG	1730
Qy	1729	TCGAGTTTAAAAACGTTCTAGSCCCCGAACCACCGGGAAGTGTCTTCTTTTAAAAA	1788
Dd	1731	TCGAGTTTAAAAACGTTCTAGSCCCCGAACCACCGGGAAGTGTCTTCTTTTAAAAA	1790
Qy	1789	CACGATAATACCATG-----	1803
Dd	1791	CACGATAATACCATGACCGGGAGATGCGAGCATGTCGGAGGCGCGTTCGTAGT	1850
Qy	1804	-----	1803
Dd	1851	CTGATFACTTTGACCTTGTACCGCACTATAAGTGTCTCTCGTAGGCTCATATGTTGG	1910
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Dd	1911	TTACATATTTTATTCACCGAGGCGAGGACACATTGCAAGTGTGGATCCCCCCCCCTCAAC	1970
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Dd	1971	GTTTCGGGGGCGCGGATGCCGTCTCTCTCCTCAGTGGCGCATCCACCCAGAGTAATC	2030
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Dd	2031	TTTACCATCAAAAAATCTTGTCTGCCATCTCGGTCCAATCTCATGTGCTCCAGGCTGCT	2090
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Qy	1804	-----	1803
Dd	2151	CGGAAGTGTGTCGGGGTCAATATGTCCAAATGCTCTCATGAAGTTCGCCGCACTGACA	2210
Qy	1804	-----	1803
Dd	2211	GGTACGTACGTTTATGATCACTCTCACCCACTGCGGACTGGGCCACCGGGCTACGA	2270
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Dd	2271	GACCTTCGGTGGCAGTTGAGCCCGTCTTCTCTGATATGGAGACCAAGTTTATCACC	2330
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Dd	2331	TGGGGGCGACACACCGCGCGGTGTGGGACATCATCTTGGGCTGCGCCGCTCCGCCGC	2390
Qy	1804	-----	1803
Dd	2391	AGGGGAGGGAGATACATCTGGGACCGGACAGACAGCCCTTGAAGGCGAGGCTGCGGACTC	2450
Qy	1804	-----GCGCTTATTACGGCTACTCCACACAGCGGAGGCTACTTGTGCTGATCATCACT	1860
Dd	2451	CTCGGCTTATTACGGCTACTCCCAACAGACGCGAGGCTACTTGTGCTGATCATCACT	2510
Qy	1861	AGCCTCACAGCGCGGACAGAAACAGGTGAGGGGAGGTCCAAAGTGTCTCCACCGCA	1920
Dd	2511	AGCCTCACAGCGCGGACAGAAACAGGTGAGGGGAGGTCCAAAGTGTCTCCACCGCA	2570
Qy	1921	ACACATCTTTCTGCGGACCTCGCTCAATGGCGTGTGTTGGACTGTCTATCATGTTGCC	1980
Dd	2571	ACACATCTTTCTGCGGACCTCGCTCAATGGCGTGTGTTGGACTGTCTATCATGTTGCC	2630
Qy	1981	GGCTCAAGAGACCTTCCCGGCCCAAGGGCCCAATCACCCAAATGTACACCAATGTGGAC	2040
Dd	2631	GGCTCAAGAGACCTTCCCGGCCCAAGGGCCCAATCACCCAAATGTACACCAATGTGGAC	2690
Qy	2041	CAGGACCTCGTTCGCTGGCAAGCGCCCGCGGCGCTTCTTGTGACCATGCACTGCTC	2100
Dd	2691	CAGGACCTCGTTCGCTGGCAAGCGCCCGCGGCGCTTCTTGTGACCATGCACTGCTC	2750
Qy	2101	GGCAGCTCGGACCTTATCTTGTGTCAGAGGCAATGCCGATGTCTATTCGGTGCCTGCGG	2160
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4321 TTTAAGGTCTATGAGCGGCGGAGATGCCCTCCACCGAGGACCTGGTTAACTCTCTCTGCT 4380

Dd	4971	TTTAAAGGTCAAGCGGGGAGATGCCCTCCACCGAGGACCTGTGTTAAACCTACTCCCTGCT	5030
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Dd	5031	ATCCTCTCCCTGGCGCCCTAGTCTCGGGGTCGTGTCGACGAGCATCTCGTTCGGCAC	5090
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Dd	5091	GTGGGCCAAGGGAGGGGGCTGTGCAGTGGATGAACCGGCTGATAGCGTTTCGCGG	5150
Qy	4501	GGTAAACACAGCTCTCCCGACGACATATGCTGAGAGGAGCGCTGACGACGTTCACT	4560
Dd	5151	GGTAAACACAGCTCTCCCGACGACATATGCTGAGAGGAGCGCTGACGACGTTCACT	5210
Qy	4561	CAGATCCTCTCTAGTCTTACCATCACTCAGTGTCTGAAGAGGCTTACACAGTGGATCAAC	4620
Dd	5211	CAGATCCTCTCTAGTCTTACCATCACTCAGTGTCTGAAGAGGCTTACACAGTGGATCAAC	5270
Qy	4621	GAGACTGCTCCAGCCCATGCTCCGGCTCGTGGCTTAAAGATGTTTGGGATTTGGATATGC	4680
Dd	5271	GAGACTGCTCCAGCCCATGCTCCGGCTCGTGGCTTAAAGATGTTTGGGATTTGGATATGC	5330
Qy	4681	ACGGTGTGACTGATTTCAAGACCTGCTCCAGTCCCAAGCTCTGCGCGGCGACGGCATCATG	4800
Dd	5331	ACGGTGTGACTGATTTCAAGACCTGCTCCAGTCCCAAGCTCTGCGCGGCGACGGCATCATG	4860
Qy	4741	GTCCCTTCTTCTCATGTCAAGTGGGTACAAAGGAGTCTGCGCGGCGACGGCATCATG	4920
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Qy	4801	CAAAACACCTGCTGAGAGCAAGATCAACCGGACATGTGAAACCGTTCATGAGG	5040
Dd	5451	CAAAACACCTGCTGAGAGCAAGATCAACCGGACATGTGAAACCGTTCATGAGG	5100
Qy	4861	ATCGTGGGGCTACGACTGATGAACACGTCGACATGGAACATTTCCCATTTAAACCGCTAC	5160
Dd	5511	ATCGTGGGGCTACGACTGATGAACACGTCGACATGGAACATTTCCCATTTAAACCGCTAC	5220
Qy	4921	ACCAACGGGCTGACAGCTCCCGGCGCAAAATTTCTAGGGGCTGTGGCGGCTG	5280
Dd	5571	ACCAACGGGCTGACAGCTCCCGGCGCAAAATTTCTAGGGGCTGTGGCGGCTG	5340
Qy	4981	GCTGCTGAGAGTACGTCGAGGTTACGCGGGTGGGGATTTCCACTACGTGACGGGCATG	5400
Dd	5631	GCTGCTGAGAGTACGTCGAGGTTACGCGGGTGGGGATTTCCACTACGTGACGGGCATG	5460
Qy	5041	ACCACTGACAAAGTAAAGTCCCGGCGCAAAATTTCTAGGGGCTGTGGCGGCTG	5520
Dd	5691	ACCACTGACAAAGTAAAGTCCCGGCGCAAAATTTCTAGGGGCTGTGGCGGCTG	5580
Qy	5101	GATGGGTGCGGTGACAGTACGCTCCAGCGTGCAAAACCCCTCTACGGGAGGCTC	5640
Dd	5751	GATGGGTGCGGTGACAGTACGCTCCAGCGTGCAAAACCCCTCTACGGGAGGCTC	5700
Qy	5161	ACATTCCTGTCGGGCTCAATCAATACCTGGTGGGTGTCAGAGTCCCATGCGAGCCGAA	5760
Dd	5811	ACATTCCTGTCGGGCTCAATCAATACCTGGTGGGTGTCAGAGTCCCATGCGAGCCGAA	5820
Qy	5221	CCGAGCTAGAGTACGTCATCTCATGCTCAGCGACCCCTCCACATTAAGCGGAGACG	5880
Dd	5871	CCGAGCTAGAGTACGTCATCTCATGCTCAGCGACCCCTCCACATTAAGCGGAGACG	5940
Qy	5281	GCTAAGCGTAGGCTGGCCAGGGATCTCCCGCTCTCTGCGGAGCTCATCAGCTAGCCAG	5990
Dd	5931	GCTAAGCGTAGGCTGGCCAGGGATCTCCCGCTCTCTGCGGAGCTCATCAGCTAGCCAG	6050
Qy	5341	CTGTCTGCGGCTCTTTGAAGGCAACATGCACTACCGCTCATGCTCCCGGAGCTGAC	6110
Dd	5991	CTGTCTGCGGCTCTTTGAAGGCAACATGCACTACCGCTCATGCTCCCGGAGCTGAC	6170
Qy	5401	CTCATCGAGGCCAACCTCTGTCGGCGCAGAGATGGGCGGGAACATCAACCGCGGTGAG	6230
Dd	6051	CTCATCGAGGCCAACCTCTGTCGGCGCAGAGATGGGCGGGAACATCAACCGCGGTGAG	6290
Qy	5461	TCAGAAAATAAGTGTAGTAAATTTTGGACTCTTTCGAGCCGCTCCAAAGCGGAGGATGAG	5520
Dd	6111	TCAGAAAATAAGTGTAGTAAATTTTGGACTCTTTCGAGCCGCTCCAAAGCGGAGGATGAG	5580
Qy	5521	AGGAAAGTATCCGTTCCCGCGGAGATCTCGGGAGGTCCAGGAAATTCCTCGAGCGATG	5640
Dd	6171	AGGAAAGTATCCGTTCCCGCGGAGATCTCGGGAGGTCCAGGAAATTCCTCGAGCGATG	5700
Qy	5581	CCCATATGGGACGCGCCCGGATTAACACCTCCTCACTGTGTAGAGTCTGTGAAGGACCCGAC	5760
Dd	6231	CCCATATGGGACGCGCCCGGATTAACACCTCCTCACTGTGTAGAGTCTGTGAAGGACCCGAC	5820
Qy	5641	TACGTCCTCCCTCAGTGTGTACAGGGTGTCCATTCGCGCTCCAGGCGCCCTCCGATACCA	5880
Dd	6291	TACGTCCTCCCTCAGTGTGTACAGGGTGTCCATTCGCGCTCCAGGCGCCCTCCGATACCA	5940
Qy	5701	CCTCCACGAGGAGGAGGACGCTTGTCTGTGTCAGAAATCTACCGTGTCTTCTGCGCTTGGG	6000
Dd	6351	CCTCCACGAGGAGGAGGACGCTTGTCTGTGTCAGAAATCTACCGTGTCTTCTGCGCTTGGG	6060
Qy	5761	GAGCTCGGCAAAAGACCTTCGCGAGCTCCGAAATGTGTGCGCGCTCGACAGCGGCAACGCA	6120
Dd	6411	GAGCTCGGCAAAAGACCTTCGCGAGCTCCGAAATGTGTGCGCGCTCGACAGCGGCAACGCA	6180
Qy	5821	ACGGCTCTCTCTGACGAGCCCTCCGACGACGCGGAGGATCCGAGCTGTGAGTCTGATC	6240
Dd	6471	ACGGCTCTCTCTGACGAGCCCTCCGACGACGCGGAGGATCCGAGCTGTGAGTCTGATC	6300
Qy	5881	TCCTTCCATGCCCTTTCGCGGAGGACCGCGGAGTCCCGATCTCAGGACGCGGTCTTGG	6360
Dd	6531	TCCTTCCATGCCCTTTCGCGGAGGACCGCGGAGTCCCGATCTCAGGACGCGGTCTTGG	6420
Qy	5941	TCCTACCGTAAAGAGGAGGCTAGTGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	6480
Dd	6591	TCCTACCGTAAAGAGGAGGCTAGTGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	6540
Qy	6001	ACAGGCGCTGATACGCGCATGCGCTGCGGAGGAGGACCAAGCTGCGCCATCAATGCACTG	6600
Dd	6651	ACAGGCGCTGATACGCGCATGCGCTGCGGAGGAGGACCAAGCTGCGCCATCAATGCACTG	6660
Qy	6061	AGCAACTCTTTGCTCCCTACCAAACTTGTGTCTATGCTCAAACTCTCGAGCGCAAGC	6720
Dd	6711	AGCAACTCTTTGCTCCCTACCAAACTTGTGTCTATGCTCAAACTCTCGAGCGCAAGC	6780
Qy	6121	CTCGGCGAGAGAGGTCACCTTTGACAGACTGCGAGTCTCTGACGACCACTACCGGAC	6840
Dd	6771	CTCGGCGAGAGAGGTCACCTTTGACAGACTGCGAGTCTCTGACGACCACTACCGGAC	6900
Qy	6181	GTGCTCAAGGAGATGAAGCGGAGGCTCCACAGTTAAGGCTAACTTCTATCCGTCGAG	6960
Dd	6831	GTGCTCAAGGAGATGAAGCGGAGGCTCCACAGTTAAGGCTAACTTCTATCCGTCGAG	7020
Qy	6241	GAAGCTGTAAAGTGAAGCGGAGGCTCCACAGTTAAGGCTAACTTCTATCCGTCGAG	7080
Dd	6891	GAAGCTGTAAAGTGAAGCGGAGGCTCCACAGTTAAGGCTAACTTCTATCCGTCGAG	7140
Qy	6301	GAGCTCGGAACTTATCCAGCAAGCGGCTTAAACCATCCGCTCCGCTGCTGGAAGGACTTG	7200
Dd	6951	GAGCTCGGAACTTATCCAGCAAGCGGCTTAAACCATCCGCTCCGCTGCTGGAAGGACTTG	7260
Qy	6361	CTGGAAGACACTGAGACCAATTTGACACCACTATGCGCAAAATAAGGTTTCTGCG	7320
Dd	7011	CTGGAAGACACTGAGACCAATTTGACACCACTATGCGCAAAATAAGGTTTCTGCG	7380
Qy	6421	GTCCAAACGAGAGAGGCGGCGGAGCTGCGCTTATTCGTTATTCGAGATTTTGGG	7440
Dd	7071	GTCCAAACGAGAGAGGCGGCGGAGCTGCGCTTATTCGTTATTCGAGATTTTGGG	7500
Qy	6481	GTTCTGTGTGCGAGAAAATGGCCCTTTTACGATGTGCTTCCACCCCTCCCTCAGGCGGTG	7560
Dd	7131	GTTCTGTGTGCGAGAAAATGGCCCTTTTACGATGTGCTTCCACCCCTCCCTCAGGCGGTG	7620

QY	6541	ATGGGCTCTTATACGAGTTCATTAATCTCTCTGACACGCGGTGAGTTCCTGGTGAAT	6600
Db	7191	ATGGGCTCTTATACGAGTTCATTAATCTCTCTGACACGCGGTGAGTTCCTGGTGAAT	7250
QY	6601	GCTTGGAAAGCGAAGAAATGCGCTATGCGCTTTCGATATGACACCGCGCTTTTGAATCA	6660
Db	7251	GCTTGGAAAGCGAAGAAATGCGCTATGCGCTTTCGATATGACACCGCGCTTTTGAATCA	7310
QY	6661	ACGGTCACTGAGAAATGACATCCGCTGTTGAGGAGTCAATCTACAAATGTTGACATGGCC	6720
Db	7311	ACGGTCACTGAGAAATGACATCCGCTGTTGAGGAGTCAATCTACAAATGTTGACATGGCC	7370
QY	6721	CCCGAAGCCAGACAGCCATAGGCTTCGCTCACAGAGCGGCTTTACATCGGGGGCCCCCTG	6780
Db	7371	CCCGAAGCCAGACAGCCATAGGCTTCGCTCACAGAGCGGCTTTACATCGGGGGCCCCCTG	7430
QY	6781	ACTAATTTCTAAAGGCGAGAACTGCGGCTATGCGCGGTGCGCGCGAGCGGTTACTGACG	6840
Db	7431	ACTAATTTCTAAAGGCGAGAACTGCGGCTATGCGCGGTGCGCGCGAGCGGTTACTGACG	7490
QY	6841	ACGAGTGGGTAATACCTCTACATGTTACTTTGAAGCGCGCTGCGGCGTGTGAGCTGG	6900
Db	7491	ACGAGTGGGTAATACCTCTACATGTTACTTTGAAGCGCGCTGCGGCGTGTGAGCTGG	7550
QY	6901	AAGCTCCAGGACTGACAGATGCTCGTATGCGGAGACGACCTTGTCTGTTATCTGTGAAGC	6960
Db	7551	AAGCTCCAGGACTGACAGATGCTCGTATGCGGAGACGACCTTGTCTGTTATCTGTGAAGC	7610
QY	6961	GGGGGACCCAGAGACAGAGGAGCCCTACGGGCTTTCACGGAGCGTATGACTAGATAC	7020
Db	7611	GGGGGACCCAGAGACAGAGGAGCCCTACGGGCTTTCACGGAGCGTATGACTAGATAC	7670
QY	7021	TCTGCCCCCTTGGGACCGCCCAACAGAGATACGACTTGGAGTGTGATAACATCATGC	7080
Db	7671	TCTGCCCCCTTGGGACCGCCCAACAGAGATACGACTTGGAGTGTGATAACATCATGC	7730
QY	7081	TCTTCCAAATGTGTCAGTCGCGACGATGCTATGCGCAAAAGGGTGTACTATCTCAACCGT	7140
Db	7731	TCTTCCAAATGTGTCAGTCGCGACGATGCTATGCGCAAAAGGGTGTACTATCTCAACCGT	7790
QY	7141	GACCCACCAACCCCTTGGCGGGGTGCGTGGGAGACAGCTAGACACATCCAGTCAAT	7200
Db	7791	GACCCACCAACCCCTTGGCGGGGTGCGTGGGAGACAGCTAGACACATCCAGTCAAT	7850
QY	7201	TCTTGGCTAGGCAACATCATGATGTCGCCACCTTGTGGCAAGGATGATCTCTGATG	7260
Db	7851	TCTTGGCTAGGCAACATCATGATGTCGCCACCTTGTGGCAAGGATGATCTCTGATG	7910
QY	7261	ACTCATTTCTTCTCCATCTTCTAGCTCAGGAAACAACTTGAAAAAGCCCTAGATTGTGAG	7320
Db	7911	ACTCATTTCTTCTCCATCTTCTAGCTCAGGAAACAACTTGAAAAAGCCCTAGATTGTGAG	7970
QY	7321	ATCTACGGGCGCTGTACTCCATGAGCAGCTTGAACCTACCTCAGATCATCAACGACTC	7380
Db	7971	ATCTACGGGCGCTGTACTCCATGAGCAGCTTGAACCTACCTCAGATCATCAACGACTC	8030
QY	7381	CATGGCCCTTAGCGCAATTTTCACTCCATGATTTACTCTCCAGGTGAGATCAATAGGTGGCT	7440
Db	8031	CATGGCCCTTAGCGCAATTTTCACTCCATGATTTACTCTCCAGGTGAGATCAATAGGTGGCT	8090
QY	7441	TCATGCGCTCAGGAAACTTGGGGTACCGCCCTTTCGAGTCTGGAGACATCGGGCGAGAAGT	7500
Db	8091	TCATGCGCTCAGGAAACTTGGGGTACCGCCCTTTCGAGTCTGGAGACATCGGGCGAGAAGT	8150
QY	7501	GTCGCGCTAGGCTTACTGTCCAGGGGGGAGGGCTGCCACTGTGGCAAGTACTCTTTC	7560
Db	8151	GTCGCGCTAGGCTTACTGTCCAGGGGGGAGGGCTGCCACTGTGGCAAGTACTCTTTC	8210
QY	7561	AACCTGGGAGTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGGGTCCCAAGTTGGAT	7620
Db	8211	AACCTGGGAGTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGGGTCCCAAGTTGGAT	8270
QY	7621	TTATCCAGCTGGTTCGTTGGTTACAGCGGGGGAGACATATATCAAGCCTGTCTCGT	7680

Db	8271	TTATCCAGCTGGTTCGTTGGTTACAGCGGGGGAGACATATATCAAGCCTGTCTCGT	8330
QY	7681	GCCCGACCCCGCTGGTTCATGTGGTGCCTACTCTCTACTTTCTGTAGGGTAGGCATCTAT	7740
Db	8331	GCCCGACCCCGCTGGTTCATGTGGTGCCTACTCTCTACTTTCTGTAGGGTAGGCATCTAT	8390
QY	7741	CTACTCCCAACCCGATGAACCGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTT	7800
Db	8391	CTACTCCCAACCCGATGAACCGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTT	8450
QY	7801	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
Db	8451	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	8510
QY	7861	TTTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
Db	8511	TTTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	8570
QY	7921	TAGCTGTGAAGCTCCGTGAGCGCTTGACTGCGAGAGTGTGATGCTGCTCTCTG	7980
Db	8571	TAGCTGTGAAGCTCCGTGAGCGCTTGACTGCGAGAGTGTGATGCTGCTCTCTG	8630
QY	7981	AGATCAAGT 7989	
Db	8631	AGATCAAGT 8639	

RESULT 9

US-10-029-907-24  
; Sequence 24, Application US/10029907  
; Patent No. 6706874  
; GENERAL INFORMATION:  
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; FILE REFERENCE: 13/083  
; CURRENT APPLICATION NUMBER: US/10/029,907  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,857  
; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 8638  
; TYPE: DNA  
; ORGANISM: HCV  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1802)... (8407)  
US-10-029-907-24

Query Match	91.0%	Score	7272.8	DB 4	Length	8638		
Best Local Similarity	92.2%	Pred. No. 0						
Matches 7975	Conservative	0	Mismatches	2	Indels	671	Gaps	3
Qy	2	CCAGCCCCGATTTGGGGGCGACACTCCACCATAGATCACTCCCTCTGTGAGGAACACTACTGT	61					
Db	2	CCAGCCCCCGATTTGGGGGCGACACTCCACCATAGATCACTCCCTCTGTGAGGAACACTACTGT	61					
Qy	62	CTTCAGCGAGAAAGCGTCTAGCCATGGCGTTAGTATGATGCTGTCAGCCTCCAGGACC	121					
Db	62	CTTCAGCGAGAAAGCGTCTAGCCATGGCGTTAGTATGATGCTGTCAGCCTCCAGGACC	121					
Qy	122	CCCCCTCCCCGGGAGAGCCATAGTGGTCTGCGGAAACCGGTGAGTACACCGGAATTGCCAGG	181					
Db	122	CCCCCTCCCCGGGAGAGCCATAGTGGTCTGCGGAAACCGGTGAGTACACCGGAATTGCCAGG	181					
Qy	182	ACGACCGGGTCTTTCTTTGGATCAACCGCTCAATGCTTGGAGATTTGGGCGTGCCTCCCG	241					
Db	182	ACGACCGGGTCTTTCTTTGGATCAACCGCTCAATGCTTGGAGATTTGGGCGTGCCTCCCG	241					
Qy	242	CGAGACTGCTAGCCGAGTAGTGTGTTGGTTCGCGAAAGGCCCTTGTGGTACTGCTGTATAGGG	301					

Db 242 |||||CGAGACTGCTACCGAGTAGTGTGGTGCAGAAAGGCGCTTGTGTACTGCTGATAGG 301  
QY 302 TGTCTTGCAGTCCCGGGAGTCTCGTAGACCGTGCACCATGACGACGAATCCTAACC 361  
Db 302 TGTCTTGCAGTCCCGGGAGTCTCGTAGACCGTGCACCATGACGACGAATCCTAACC 361  
QY 362 TCAAGAAACCAAGGCGCGCCATGATTGAACAAGATGATTGCAACGAGTCTCC 421  
Db 362 TCAAGAAACCAAGGCGCGCCATGATTGAACAAGATGATTGCAACGAGTCTCC 421  
QY 422 GCGCGTGGTGGAGAGCTATTCCGCTATGACTGAGGGAACAAGATGATTGCAACGAGTCTCC 481  
Db 422 GCGCGTGGTGGAGAGCTATTCCGCTATGACTGAGGGAACAAGATGATTGCAACGAGTCTCC 481  
QY 482 TGATGCCCGCTGTTCGGCTGTGACGCGAGGGCGCGGCTTCTTTTGTCAAGACGA 541  
Db 482 TGATGCCCGCTGTTCGGCTGTGACGCGAGGGCGCGGCTTCTTTTGTCAAGACGA 541  
QY 542 CTTGTCCGCTGCTGAATGAACTGACGAGGAGCGGCTATCGTGGCTGCCAC 601  
Db 542 CTTGTCCGCTGCTGAATGAACTGACGAGGAGCGGCTATCGTGGCTGCCAC 601  
QY 602 GACGGGCTTCTTCCGCGAGCTGCTCGACGTTGTCTACTGAGCGGAGGAGCTGGCT 661  
Db 602 GACGGGCTTCTTCCGCGAGCTGCTCGACGTTGTCTACTGAGCGGAGGAGCTGGCT 661  
QY 662 GCTATTGGGCGAAGTGCAGGCGGAGGATCTCTGTGCTATCTACCTTGTCTTCCGCGGAA 721  
Db 662 GCTATTGGGCGAAGTGCAGGCGGAGGATCTCTGTGCTATCTACCTTGTCTTCCGCGGAA 721  
QY 722 AGTATCCATGCTGATGCAATGCGCGGCTGATACGCTGATCGGCTACCTGCC 781  
Db 722 AGTATCCATGCTGATGCAATGCGCGGCTGATACGCTGATCGGCTACCTGCC 781  
QY 782 ATTGCACCAAGGAGAACTGCTGACGAGGAGCAGTACTCGGATGGAAGCGGTCT 841  
Db 782 ATTGCACCAAGGAGAACTGCTGACGAGGAGCAGTACTCGGATGGAAGCGGTCT 841  
QY 842 TGTGATCAGGATGATCTGACGAGGAGCAGGAGTCTCGTGACCCATGCGGAGCTGTCG 901  
Db 842 TGTGATCAGGATGATCTGACGAGGAGCAGGAGTCTCGTGACCCATGCGGAGCTGTCG 901  
QY 902 CAGGCTCAAGCGCGCATGCGCGAGGAGTCTCGTGACCCATGCGGAGCTGTCG 961  
Db 902 CAGGCTCAAGCGCGCATGCGCGAGGAGTCTCGTGACCCATGCGGAGCTGTCG 961  
QY 962 CTTGCGGAATATCATGTTGGAATGCGGCTTCTGGAATCATGACTGTCGCGGT 1021  
Db 962 CTTGCGGAATATCATGTTGGAATGCGGCTTCTGGAATCATGACTGTCGCGGT 1021  
QY 1022 GGTGTGCGGAGCGGCTATCAGGACATAGCGTTCGGTACCGGTGATATGCTGAAGAGCT 1081  
Db 1022 GGTGTGCGGAGCGGCTATCAGGACATAGCGTTCGGTACCGGTGATATGCTGAAGAGCT 1081  
QY 1082 TGGCGGGAATGGGCTGACGCTTCTGCTGTTTACGATGCGGCTCCCGATTCGCA 1141  
Db 1082 TGGCGGGAATGGGCTGACGCTTCTGCTGTTTACGATGCGGCTCCCGATTCGCA 1141  
QY 1142 GCGATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTT-----TAAAC 1189  
Db 1142 GCGATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTT-----TAAAC 1189  
QY 1190 AGACCAACAGGTTTCCCTCTAGCGGATCAATTCGCGGCTTCTCCCTCCCGCCCTTA 1249  
Db 1202 AGACCAACAGGTTTCCCTCTAGCGGATCAATTCGCGGCTTCTCCCGCCCTTA 1250  
QY 1250 ACCTTACTGCGGAGCGGCTTGAATGAGCGGCTGTCGCTTGTCTATATGTTATTT 1309  
Db 1251 ACCTTACTGCGGAGCGGCTTGAATGAGCGGCTGTCGCTTGTCTATATGTTATTT 1310  
QY 1310 CCACCATATTGCGCTTCTTTGGCAATGTGAGGCGCGGAACTTGGCCCTGTCTTTTGA 1369

Db 1311 CCACCATATTGCGCTCTTTTGGCAATGTGAGGCGCGGAAACCTTGGCCCTGTCTTTTGA 1370  
QY 1370 CGAGCATTTCTAGGGTCTTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCG 1429  
Db 1371 CGAGCATTTCTAGGGTCTTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCG 1430  
QY 1430 TGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGCAACACACGCTCTGTAGGACCTTT 1489  
Db 1431 TGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGCAACACACGCTCTGTAGGACCTTT 1490  
QY 1490 GAGGACGCGAACCCCTCTCAAGCGTATTCAACAGGGCTGAAGATGCCAGAAAG 1549  
Db 1491 GAGGACGCGAACCCCTCTCAAGCGTATTCAACAGGGCTGAAGATGCCAGAAAG 1550  
QY 1550 AAGATACACCTGCAAGGGCGGCAACCCCTCTCAAGCGTATTCAACAGGGCTGAAGATGCCAGAAAG 1609  
Db 1551 AAGATACACCTGCAAGGGCGGCAACCCCTCTCAAGCGTATTCAACAGGGCTGAAGATGCCAGAAAG 1610  
QY 1610 AAAGAGTCAAAATGGCTCTCTCAAGCGTATTCAACAGGGCTGAAGATGCCAGAAAG 1669  
Db 1611 AAAGAGTCAAAATGGCTCTCTCAAGCGTATTCAACAGGGCTGAAGATGCCAGAAAG 1670  
QY 1670 TACCCATTTATGGGATCTGATCTGGGCGCTCGGTGACATGCTTTTACATGTTTGTAGT 1729  
Db 1671 TACCCATTTATGGGATCTGATCTGGGCGCTCGGTGACATGCTTTTACATGTTTGTAGT 1730  
QY 1730 CGAGGTTAAAAACGCTTAGGCGCGGCAACCCCTCTCAAGCGTATTCAACAGGGCTGAAGATGCCAGAAAG 1789  
Db 1731 CGAGGTTAAAAACGCTTAGGCGCGGCAACCCCTCTCAAGCGTATTCAACAGGGCTGAAGATGCCAGAAAG 1790  
QY 1790 ACGATAATACCATG----- 1803  
Db 1791 ACGATAATACCATGCGGAGATGCGAGCATCGTGGGAGGCGGCTTTTTCGTAGTCC 1850  
QY 1804 ----- 1803  
Db 1851 TGATACTCTTGACCTTGTACCGCACTATTAAGCTGTTCTCGCTAGGCTCATATGTTGT 1910  
QY 1804 ----- 1803  
Db 1911 TACAATATTTTATCACCAGGCGCGGAGCACACTTGAAGTGTGATCCCGGCTCAACG 1970  
QY 1804 ----- 1803  
Db 1971 TTGGGGGGCGCGATGCGCTCATCTCTCTCAGTGGCGATCCACCGAGAGTAATCT 2030  
QY 1804 ----- 1803  
Db 2031 TTACCATCACCAAAATCTTGTGCGCCATACTCGGTCCACTCATGTTGCTCCAGGCTGTA 2090  
QY 1804 ----- 1803  
Db 2091 TAACCAAGTGGCTACTTCTGCGGCAACCGGCTCATTTCTGTCATGTCATGCTGTCG 2150  
QY 1804 ----- 1803  
Db 2151 GGAAGTTGTGGGGTCAATATGTCAAATGGCTCTCATGAAGTTGGCGGCTGACAG 2210  
QY 1804 ----- 1803  
Db 2211 GTAGTACGTTTATGACCATCTCACCCACTGCGGGACTGCGGCCACCGCGGCTACGAG 2270  
QY 1804 ----- 1803  
Db 2271 ACCTTGGGTGGAGTTGAGCCCGTGTCTTCTCTGATATGAGAGCAAGGTTATACCT 2330  
QY 1804 ----- 1803  
Db 2331 GGGGGGAGACCGCGGCGGTGTGGGAGCATCATCTTGGGCTTGCCTGCTCCGCGCGCA 2390  
QY 1804 ----- 1803  
Db 2391 GGGGGAGGAGATACATCTGGGACCGGACAGCCCTTGAGGGCAGGGGTGGGACTCC 2450

QY	1804	--GCGCCTATTACGGCCTACTCCACAGACGGCGCCTACTTGGCTCATCATCACTA	1861	QY	2882	AGGGGGGAGGACCACTCTTTCTCCATTCCAAAGAAATGTGATGAGCTCGCGCGA	2941
Db	2451	TCGCGCCTATTACGGCCTACTCCACAGACGGCGCCTACTTGGCTCATCATCACTA	2510	Db	3531	AGGGGGGAGGACCACTCTTTCTCCATTCCAAAGAAATGTGATGAGCTCGCGCGA	3590
QY	1862	GCTCACAGCGCGGACAGAAACAGGTCCAGGGGAGGTCCAAAGTGTCTCCACCGCAA	1921	QY	2942	AGCTGTCCGGCTTCGGACTCAATGCTGTAGCATATTACCGGGCCCTTGATGTATCGTCA	3001
Db	2511	GCTCACAGCGCGGACAGAAACAGGTCCAGGGGAGGTCCAAAGTGTCTCCACCGCAA	2570	Db	3591	AGCTGTCCGGCTTCGGACTCAATGCTGTAGCATATTACCGGGCCCTTGATGTATCGTCA	3650
QY	1922	CACAATCTTCTCGCGAAGCTCGCTCAATGGCGTGTGTGGACTGTCTATCATGTGCGG	1981	QY	3002	TACCAACTAGCGGAGACGTCATTGTCTAGCAACGAGCCTCTAAATGACGGGCTTTACCG	3061
Db	2571	CACAATCTTCTCGCGAAGCTCGCTCAATGGCGTGTGTGGACTGTCTATCATGTGCGG	2630	Db	3651	TACCAACTAGCGGAGACGTCATTGTCTAGCAACGAGCCTCTAAATGACGGGCTTTACCG	3710
QY	1982	GCTCAAGACCTTTCGGGCGCCAAAGGCGCCATCACCCAAATGTACCAATGTGGAC	2041	QY	3062	GGGATTTCCACTCAGTGATCGACTGCAATACATGTGTACCCAGACAGTCGACTCAGCC	3121
Db	2631	GCTCAAGACCTTTCGGGCGCCAAAGGCGCCATCACCCAAATGTACCAATGTGGAC	2690	Db	3711	GGGATTTCCACTCAGTGATCGACTGCAATACATGTGTACCCAGACAGTCGACTCAGCC	3770
QY	2042	AGGACCTCGTTCGGCTCGGCAAGCGCCCGGGGCGGTTCTTTGACACCATGCACCTGGC	2101	QY	3122	TGGAACCGGACCTTCACTTACCATTTGAGACGACCGTGCACCAAGACGGGTGTACGCTCGC	3181
Db	2691	AGGACCTCGTTCGGCTCGGCAAGCGCCCGGGGCGGTTCTTTGACACCATGCACCTGGC	2750	Db	3771	TGGAACCGGACCTTCACTTACCATTTGAGACGACCGTGCACCAAGACGGGTGTACGCTCGC	3830
QY	2102	CGAGCTCGACCTTTACTTGGTCAAGAGGATGCCGATGTCAATCCGGTGCAGCGCGGG	2161	QY	3182	AGCGGCGAGGACGAGTGGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGAG	3241
Db	2751	CGAGCTCGACCTTTACTTGGTCAAGAGGATGCCGATGTCAATCCGGTGCAGCGCGGG	2810	Db	3831	AGCGGCGAGGACGAGTGGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGAG	3890
QY	2162	CGGACAGGAGGAGGAGCTACTCTCCCGGCGCGCTCTCTCTACTTTGAGGGGCTCTTCGG	2221	QY	3242	AAGCGCCCTCGGCGATGTTTCGATTTCTCGGTTCTGTGAGTGTCTATGACCGGGGCTGTG	3301
Db	2811	CGGACAGGAGGAGGAGCTACTCTCCCGGCGCGCTCTCTCTACTTTGAGGGGCTCTTCGG	2870	Db	3891	AAGCGCCCTCGGCGATGTTTCGATTTCTCGGTTCTGTGAGTGTCTATGACCGGGGCTGTG	3950
QY	2222	GCGGCTCACTGCTCTGCGGCTCGGGGCAAGCTGTGGGCACTTTTCGGGCTGCGGTGTGCA	2281	QY	3302	CTTGTGACGAGCTACGCGCGGCGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACAC	3361
Db	2871	GCGGCTCACTGCTCTGCGGCTCGGGGCAAGCTGTGGGCACTTTTCGGGCTGCGGTGTGCA	2930	Db	3951	CTTGTGACGAGCTACGCGCGGCGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACAC	4010
QY	2282	CCGAGGGGTTGCGAAGCGGTGGACTTTGTAACCGTTCGAGTCTATGGAAACCACTATGC	2341	QY	3362	CAGGGTTGCGGCTCTGCCAGGACCATCTGGAGTTCTGGGAGAGCGTCTTTTACAGGGCTCA	3421
Db	2931	CCGAGGGGTTGCGAAGCGGTGGACTTTGTAACCGTTCGAGTCTATGGAAACCACTATGC	2990	Db	4011	CAGGGTTGCGGCTCTGCCAGGACCATCTGGAGTTCTGGGAGAGCGTCTTTTACAGGGCTCA	4070
QY	2342	GCTCCGGGCTTCAGGCAACCTCGTCCCTCGGGCGTACCGGACACATTCAGGTGG	2401	QY	3422	CCACATAGACGCCCATTTCTTCCAGACTAAGCAGGAGGAGAGCAACTTTCCTTACC	3481
Db	2991	GCTCCGGGCTTCAGGCAACCTCGTCCCTCGGGCGTACCGGACACATTCAGGTGG	3050	Db	4071	CCACATAGACGCCCATTTCTTCCAGACTAAGCAGGAGGAGAGCAACTTTCCTTACC	4130
QY	2402	CCCATCTACACGCGCCTTACTGTAGCGGCAAGAGCACTAAGGTGCGGCTGCGTATGCG	2461	QY	3482	TGCTAGCATACGAGGCTACGGTGTGCGCGGAGGCTCAGGCTCCACCTCCATCGTGGAGC	3541
Db	3051	CCCATCTACACGCGCCTTACTGTAGCGGCAAGAGCACTAAGGTGCGGCTGCGTATGCG	3110	Db	4131	TGCTAGCATACGAGGCTACGGTGTGCGCGGAGGCTCAGGCTCCACCTCCATCGTGGAGC	4190
QY	2462	CCCAAGGGTATAAGGTGCTTGTCTGAAACCGGTCGCGCGCCACCCCTAGGTTTCGGGG	2521	QY	3542	AAATGTGGAAAGTGTCTCATACGGCTAAAGCTACGCTGCAACGCGGCCAAACCCCTCTGT	3601
Db	3111	CCCAAGGGTATAAGGTGCTTGTCTGAAACCGGTCGCGCGCCACCCCTAGGTTTCGGGG	3170	Db	4191	AAATGTGGAAAGTGTCTCATACGGCTAAAGCTACGCTGCAACGCGGCCAAACCCCTCTGT	4250
QY	2522	CGTATATGCTAAGGCACATGGTATCGACCTTAACATCAGAACCGGGTTAAGGACCATCA	2581	QY	3602	ATAGGCTGGGAGCGGCTTCAAAACGAGGTTACTACACACACACCCCATTAACCAATACATCA	3661
Db	3171	CGTATATGCTAAGGCACATGGTATCGACCTTAACATCAGAACCGGGTTAAGGACCATCA	3230	Db	4251	ATAGGCTGGGAGCGGCTTCAAAACGAGGTTACTACACACACACCCCATTAACCAATACATCA	4310
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QY	2642	CTGGGGCGGCTATGACATCATATATGATGATGTCGCACTCAACTGACTCGACCATCA	2701	QY	3722	TCCTAGCAGCTCTGGCGCGCTATTGCTGTGACACAGGACGAGTGTGTCTTGTGGGAGGA	3781
Db	3291	CTGGGGCGGCTATGACATCATATATGATGATGTCGCACTCAACTGACTCGACCATCA	3350	Db	4371	TCCTAGCAGCTCTGGCGCGCTATTGCTGTGACACAGGACGAGTGTGTGTGGGAGGA	4430
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RESULT 10
US-10-029-907-7
; Sequence 7, Application US/10029907
; Patent No. 6706874
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; TITLE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/029,907
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
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; NAME/KEY: CDS									
; LOCATION: (1802) ... (8407)									
US-10-029-907-7									
Query Match 90.7%; Score 7249.8; DB 4; Length 8638;									
Best Local Similarity 92.0%; Pred. No. 0;									
Matches 7961; Conservative 0; Mismatches 17; Indels 671; Gaps 3;									
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Qy	841	TTGTTCGATCAGGATGATCTGACGAAAGAGCATCAGGGGCTCGCGCAGCCGAACTGTTGC	900						
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Qy	961	GCTTGGCGAATATATGTTGGTGGAAATGGCGCTTTTCTGGATTATCGACTGTGGCGGC	1020						
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Qy	1249	AACGTTACTGGCGGACCGCTTGGATTAAGGCGGTGCGTTGTCTATATGTTATTT	1308						
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Qy	1309	TCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCGCGGAAACCTGSCCTGTCTCTTG	1368						
Db	1310	TCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCGCGGAAACCTGSCCTGTCTCTTG	1369						
Qy	1369	ACGAGCATCTTAGGGTCTTTTCCCTCTCGCMAAGGAATGCAAGTCTGTGAATGTC	1428						
Db	1370	ACGAGCATCTTAGGGTCTTTTCCCTCTCGCMAAGGAATGCAAGTCTGTGAATGTC	1429						
Qy	1429	GTGAAGCAAGCAGTTCCTCTGGAGCTCTTGAGACAAACAGTCTGTAGCACCTTT	1488						
Db	1430	GTGAAGCAAGCAGTTCCTCTGGAGCTCTTGAGACAAACAGTCTGTAGCACCTTT	1489						
Qy	1489	TGCAGGCGAGCGGAACCCCTGCGGACAGGTGCTCTGCGGCCAAAAGCCACGTTA	1548						
Db	1490	TGCAGGCGAGCGGAACCCCTGCGGACAGGTGCTCTGCGGCCAAAAGCCACGTTA	1549						
Qy	1549	TAAGATACACTGCAAGGCGGCAACCCCGAGTGCACCGTGTGAGTGGATAGTTGTG	1608						
Db	1550	TAAGATACACTGCAAGGCGGCAACCCCGAGTGCACCGTGTGAGTGGATAGTTGTG	1609						
Qy	1609	GAAAGCTCAATGGCTCTCTCAAGCTATTCAACAAGGGGCTGAAGGATGCCAGAAG	1668						
Db	1610	GAAAGCTCAATGGCTCTCTCAAGCTATTCAACAAGGGGCTGAAGGATGCCAGAAG	1669						
Qy	1669	GTACCCCATTTGATGGGATCTGATCTGGGCTCTCGGTGCAACATGCTTACATGTTTAG	1728						
Db	1670	GTACCCCATTTGATGGGATCTGATCTGGGCTCTCGGTGCAACATGCTTACATGTTTAG	1729						
Qy	1729	TGAGGTTAAAAACGCTTAGGCCCCCGAAACACCGGGGACGTTGTTTCTTTGAAAAA	1788						
Db	1730	TGAGGTTAAAAACGCTTAGGCCCCCGAAACACCGGGGACGTTGTTTCTTTGAAAAA	1789						
Qy	1789	CAAGATAATACCATG-----	1803						
Db	1790	CACGATAATACCATGACCGGAGATGGCAGCATCGTGGGAGCGCGGTTTCGTAGGT	1849						
Qy	1804	-----	1803						
Db	1850	CTGATACTCTTGACCTTGTACCGCACTATAAGCTGTCTCTCGTAGGCTCATATGTTG	1909						
Qy	1804	-----	1803						
Db	1910	TTACAATATTTTATCACCAGGCGGAGGACACTTGCAGTGTGGATCCCCCCCCCTCAAC	1969						
Qy	1804	-----	1803						
Db	1970	GTTTCGGGGGGCGCGATGCCGTCTCTCTCACTGCGCGATCCACCGAGAGTAATC	2029						
Qy	1804	-----	1803						

Db 2030 TTTACCATCAACAAAATCTTGCTCGCCATCTCGGTCCACTCATGGTGTCCAGGCTGTT 2089  
Qy 1804 ----- 1803  
Db 2090 ATAACAAAGTCCGTACTTCTGTGCGCGCACACGGGCTCATTCGTGTGATGCAATGCTGGTG 2149  
Qy 1804 ----- 1803  
Db 2150 CGGAAGGTTGCTGGGGTCAATATGTCCAAATGGCTCTCATGAAGTTGGCCGCACGTGACA 2209  
Qy 1804 ----- 1803  
Db 2210 GGTACGTAGCTTTATGACCAATCTCACCCACTGCGGGACTGGGCCCAACGCGGGCTTACGA 2269  
Qy 1804 ----- 1803  
Db 2270 GACCTTGGGTGGCAGTTGAGCCCGTGTCTTCTCTGATATGGAGACCAAGGTTATCACC 2329  
Qy 1804 ----- 1803  
Db 2330 TGGGGGCGAGACACCGCGCGTGTGGGGACATCATCTTGGGCTGTCCCGTCTCCGCCCGC 2389  
Qy 1804 ----- 1803  
Db 2390 AGGGGAGGGAGATACATCTGGGACCGCGAGACAGCCTTTGAAGGGCAGGGTGGGACTC 2449  
Qy 1804 ---GCGCCTATTACGCGCTACTCCCAACAGCGAGGCGCTACTTGGCTGCATCATCACT 1860  
Db 2450 CTCGCGCCTATTACGCGCTACTCCCAACAGCGAGGCGCTACTTGGCTGCATCATCACT 2509  
Qy 1861 AGCCTCACAGCGCGGACAGGAACCAAGGTCGAGGGGGAGGTCCAAAGTGTCTCCACCGCA 1920  
Db 2510 AGCCTCACAGCGCGGACAGGAACCAAGGTCGAGGGGGAGGTCCAAAGTGTCTCCACCGCA 2569  
Qy 1921 ACACAACTTTCTGTCGCGACTGCGTCAATGAGGCTGTGTGACTGTCTATCATGTGTC 1980  
Db 2570 ACACAACTTTCTGTCGCGACTGCGTCAATGAGGCTGTGTGACTGTCTATCATGTGTC 2629  
Qy 1981 GGCTCAAGACCTTTCGCGGCCCAAGGGCCAAATCACCACCAATGACACCAATGACCAATGAGAC 2040  
Db 2630 GGCTCAAGACCTTTCGCGGCCCAAGGGCCAAATCACCACCAATGACACCAATGACCAATGAGAC 2689  
Qy 2041 CAGGACTCGTGGCTGGCAAGCGCCCGCGGGCGCTTCTTGACACCATGCACTGTC 2100  
Db 2690 CAGGACTCGTGGCTGGCAAGCGCCCGCGGGCGCTTCTTGACACCATGCACTGTC 2749  
Qy 2101 GGCAGCTCGGACTTTTACTTGTGTACAGGCAATGCGGATGTCTTCGCTGCGCGCGCG 2160  
Db 2750 GGCAGCTCGGACTTTTACTTGTGTACAGGCAATGCGGATGTCTTCGCTGCGCGCGCG 2809  
Qy 2161 GCGCAGCAGGGGAGCTTCTCTCCCGCGCGCTCTCTTACTTTGAAGGCTCTTTCG 2220  
Db 2810 GCGCAGCAGGGGAGCTTCTCTCCCGCGCGCTCTCTTACTTTGAAGGCTCTTTCG 2869  
Qy 2221 GCGGCTCCACTGCTCTGCGCTCGGGGACGCTGTGGGCACTTTTCGGGCTGCGGCTGTGC 2280  
Db 2870 GCGGCTCCACTGCTCTGCGCTCGGGGACGCTGTGGGCACTTTTCGGGCTGCGGCTGTGC 2929  
Qy 2281 ACCGAGGGGTTCGGAAGGGGTGGAATTTGTACCGCTGAGTCTATGAAACCACTATG 2340  
Db 2930 ACCGAGGGGTTCGGAAGGGGTGGAATTTGTACCGCTGAGTCTATGAAACCACTATG 2989  
Qy 2341 CGGTCCCGCTTTCACGGCAACTCGTCCCTTCGGCGGTACCGCAGACATTCACAGGTG 2400  
Db 2990 CGGTCCCGCTTTCACGGCAACTCGTCCCTTCGGCGGTACCGCAGACATTCACAGGTG 3049  
Qy 2401 GCCCATCTACGCCCTTACTGTAGCGGCAAGACACTAAGTGTGCGGCTGCGTATGCA 2460  
Db 3050 GCCCATCTACGCCCTTACTGTAGCGGCAAGACACTAAGTGTGCGGCTGCGTATGCA 3109  
Qy 2461 GCCCAGGTTAAGGCTGTCTGAAACCGCTCGTCCCGCGCACCTTAGGTTTCGGG 2520  
Db 3110 GCCCAGGTTAAGGCTGTCTGAAACCGCTCGTCCCGCGCACCTTAGGTTTCGGG 3169

Qy 2521 GCGTATATGTCTAAGGCACATGGTATCGACCCCTAAACATCAGAACCGGGTAAGGACCATC 2580  
Db 3170 GCGTATATGTCTAAGGCACATGGTATCGACCCCTAAACATCAGAACCGGGTAAGGACCATC 3229  
Qy 2581 ACCGAGGTGCGCCCATCAGCTACTCCACCTATGCGAAGTTTCTTGCAGCGGTGGTGC 2640  
Db 3230 ACCGAGGTGCGCCCATCAGCTACTCCACCTATGCGAAGTTTCTTGCAGCGGTGGTGC 3289  
Qy 2641 TCTGGGGGCGCTATGACATCATATATGTATGATGTCACCTCAACTGACTCGACCACT 2700  
Db 3290 TCTGGGGGCGCTATGACATCATATATGTATGATGTCACCTCAACTGACTCGACCACT 3349  
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Db 3470 GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGCAAGCCATCCCATCGAGACCATC 3529  
Qy 2881 AAGGGGGGAGGACCTCATTTTCTGCCATTCCAAAGAAATGTATGAGTCTGCGCG 2940  
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Qy 3001 ATACCAACTAGCGGAGAGCTCATTTCTGTAGCAAGCGGACGCTCTAATGACGGGCTTACC 3060  
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Qy 3061 GCGGATTTGACTCAGTGTATGACTGCAATATATGTGTCAACAGACAGTCTGACTTTCAGC 3120  
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Qy 3181 CAGCGCGGAGGACGACTGCTAGGGGACGATGGGCAATTTACAGGTTTGTGACTCCAGGA 3240  
Db 3830 CAGCGCGGAGGACGACTGCTAGGGGACGATGGGCAATTTACAGGTTTGTGACTCCAGGA 3889  
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Qy 3301 GCTTGTAGAGCTACGCGCCCGGAGACTCAGTTAGGTTGCGGGCTTACCTAAACACA 3360  
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QY 3721 GTCTTAGAGCTCTGGCCGCGTATTGCTTGAACAAGGAGCGTGTCTATTGTGGCAGG 3780  
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QY 3781 ATCATCTTGTCCGAAAGCGCGCATCATTCGACAGGGAATGCTTTACCGGAGTTC 3840  
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QY 3841 GATGAGATGGAAGAGTGCCTTACACCTCCCTTATCATCGACAGGGAATGAGCTCGCC 3900  
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DB ACCCTCTGTTTAAATCCTGGGGGATGGTGGCGGCCCTTCTGCTCCAGCGCT 4849  
QY 4201 GCTTCTGCTTTTCTAGGCGCGGATCGCTGAGCGGCTGTGGCAGATAGGCTTTGGG 4260  
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## RESULT 11

US-10-029-907-25  
 ; Sequence 25, Application US/10029907  
 ; Patent No. 6706874  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
 ; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
 ; FILE REFERENCE: 13/083  
 ; CURRENT APPLICATION NUMBER: 2001-12-21  
 ; CURRENT FILING DATE: 2001-12-21  
 ; PRIOR APPLICATION NUMBER: 60/257,857  
 ; PRIOR FILING DATE: 2000-12-22  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 25  
 ; LENGTH: 8638  
 ; TYPE: DNA  
 ; ORGANISM: HCV  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1802)....(8407)  
 US-10-029-907-25

Query Match 90.7%; Score 7248.8; DB 4; Length 8638;  
 Best Local Similarity 92.0%; Pred. No. 0;  
 Matches 7960; Conservative 0; Mismatches 17; Indels 671; Gaps 3;

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RESULT 12
US-10-029-907-2
; Sequence 2, Application US/10029907
; Patent No. 6706874
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; TITLE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 8642
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
; NAME/KEY: variation
; LOCATION: 6268
; OTHER INFORMATION: r = a or g
; NAME/KEY: variation
; LOCATION: 4446
; OTHER INFORMATION: r = a or g
US-10-029-907-2

Query Match 90.7%; Score 7246.8; DB 4; Length 8642;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 7966; Conservative 2; Mismatches 9; Indels 675; Gaps 4;

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D 62 CTTTACGACAGAAAGCGTTAGCCATGCGTTAGTATGAGTGTGCTGACGCTCCAGACC 121
QY 122 CCCCTTCCCGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGG 181
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RESULT 13  
US-10-029-907-6  
; Sequence 6, Application US/10029907  
; Patent No. 6706874  
; GENERAL INFORMATION:  
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
; FILE OF INVENTION: HEPATITIS C VIRUS  
; FILE REFERENCE: 13/083  
; CURRENT APPLICATION NUMBER: US/10/029,907  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,857

; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 8638  
; TYPE: DNA  
; ORGANISM: HCV  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1802)... (8407)  
US-10-029-907-6

Query Match 90.7%; Score 7245.6; DB 4; Length 8638;  
Best Local Similarity 92.0%; Pred. No. 0;  
Matches 7958; Conservative 0; Mismatches 19; Indels 671; Gaps 3;  
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Db 122 CCCCCCTCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTCGACG 181  
QY 182 ACGACCGGCTCTTTCTTTGGATCAACCCGCTCAATGCCCTGGAGATTGGGCGTGCCTCCG 241  
Db 182 ACGACCGGCTCTTTCTTTGGATCAACCCGCTCAATGCCCTGGAGATTGGGCGTGCCTCCG 241  
QY 242 CGAGACTCTAGCCGAGTAGTGTGGGTGCGGAAGGCCCTTGTGCTACTGCTGATAGGG 301  
Db 242 CGAGACTCTAGCCGAGTAGTGTGGGTGCGGAAGGCCCTTGTGCTACTGCTGATAGGG 301  
QY 302 TGTTCGAGTGCCTCCGGGAGGCTCTCGTAGACCGTGACCATGAGCAGCAATCTTAAACC 361  
Db 302 TGTTCGAGTGCCTCCGGGAGGCTCTCGTAGACCGTGACCATGAGCAGCAATCTTAAACC 361  
QY 362 TCAAGAAAAACCAAGGCGCGCCATGATTGAACAAGATGATGATGCGAGGTTCTCC 421  
Db 362 TCAAGAAAAACCAAGGCGCGCCATGATTGAACAAGATGATGATGCGAGGTTCTCC 421  
QY 422 GCGCGCTTGGTGGAGAGGCTATTGCGCTATGACTGGGCAACAGACAATCGGCTGTC 481  
Db 422 GCGCGCTTGGTGGAGAGGCTATTGCGCTATGACTGGGCAACAGACAATCGGCTGTC 481  
QY 482 TGATGCCCGCTGTTCCGGCTGTGAGCGAGGGGCGCGCGTCTTTTGTCAAGACCGA 541  
Db 482 TGATGCCCGCTGTTCCGGCTGTGAGCGAGGGGCGCGCGTCTTTTGTCAAGACCGA 541  
QY 542 CTTGTCGGTCCCTGTAATGAACTGCGAGAGCGAGCGCGGCTATCGTGGTGGCCAC 601  
Db 542 CTTGTCGGTCCCTGTAATGAACTGCGAGAGCGAGCGCGGCTATCGTGGTGGCCAC 601  
QY 602 GACGCGGCTTCTTGGCGAGCTGTGCTGAGGTTGTCTAAAGCGGGAAGGAGTGGCT 661  
Db 602 GACGCGGCTTCTTGGCGAGCTGTGCTGAGGTTGTCTAAAGCGGGAAGGAGTGGCT 661  
QY 662 GCTATTGGCGGAAGTGGCGGGCAGGATCTCTGTCATCTCACCTTGTCTTCCCGGAGAA 721  
Db 662 GCTATTGGCGGAAGTGGCGGGCAGGATCTCTGTCATCTCACCTTGTCTTCCCGGAGAA 721  
QY 722 AGTATCCATCATGGCTGATGCAATGCGCGGCTGCATACGCTTGATCCGGTACTCGGCC 781  
Db 722 AGTATCCATCATGGCTGATGCAATGCGCGGCTGCATACGCTTGATCCGGTACTCGGCC 781  
QY 782 ATTGCAACCAAGCGAAACATCCATCGAGCGAGAGGTAAGGAGCGGCT 841  
Db 782 ATTGCAACCAAGCGAAACATCCATCGAGCGAGAGGTAAGGAGCGGCT 841  
QY 842 TGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGGCCGCACTGTTCCG 901

Db	842	TGTCGATCAGGATGATCTGACGAGAGCATCAGGGCTCGCGCCAGCGAACTGTCG	901	Db	1911	TACAATATTTTATPACCAAGGCGGAGGCACATTGCAAGTGTGGATCCCCCCTCAACG	1970
Qy	902	CAGGCTCAAGGGCGCGATGCCCGACGGCAGGATCTCGTGTGTGACCCATGGCGATGCCTG	961	Qy	1804	-----	1803
Db	902	CAGGCTCAAGGGCGCGATGCCCGACGGCAGGATCTCGTGTGTGACCCATGGCGATGCCTG	961	Db	1971	TTGCGGGGGCGCGATGCCGTATCTCTCCTCAGGTGCGGATCCACCCAGAGCTAATCT	2030
Qy	962	CTTGCCGAATATCATGTTGGAAATGGCGCTTTTCTGGATTCATGACATGTGCGCGGCT	1021	Qy	1804	-----	1803
Db	962	CTTGCCGAATATCATGTTGGAAATGGCGCTTTTCTGGATTCATGACATGTGCGCGGCT	1021	Db	2031	TTACCATCACAAATCTTTGCTCGCATACTCGGTCCACTCATGTGTCTCAGGCTGGTA	2090
Qy	1022	GGGTGTGGGGACCGCTATCAGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCT	1081	Qy	1804	-----	1803
Db	1022	GGGTGTGGGGACCGCTATCAGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCT	1081	Db	2091	TAACAAAGTGGCGTACTTGTGCGCGACACAGGGGTCAATTCGTGATGATGCTGTGTCG	2150
Qy	1082	TGCGCGGAATGGGTGACCGCTTCTGCTGCTTTAGCGTATCGCGCTCCCGATTCGCA	1141	Qy	1804	-----	1803
Db	1082	TGCGCGGAATGGGTGACCGCTTCTGCTGCTTTAGCGTATCGCGCTCCCGATTCGCA	1141	Db	2151	GGNAGTTGCTGGGGTCAATTATGTCCAAATGCTCTCATGAAGTTGGCGCGACTGACAG	2210
Qy	1142	GCSCATCGCTTCTATCGCTTCTTGACGAGTTCTTCTGAGTT-----TAAAC	1189	Qy	1804	-----	1803
Db	1142	GCSCATCGCTTCTATCGCTTCTTGACGAGTTCTTCTGAGTT-----TAAAC	1189	Db	2211	GTACGTACGTTTATGACCATCTCACCCACTGCGGGACTGGGCCACGCGGGGCTACGAG	2270
Qy	1190	AGACCAACACGGTTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCCCCCCCTA	1249	Qy	1804	-----	1803
Db	1202	AGACCAACACGGTTTCCCTCTAGCGGATCAATTCGCG-----CCCCCCCCCTA	1250	Db	2271	ACCTTGGGTGGCAGTTGAGCCCGTCTTCTCTGATATGAGAGCAAGGTTATCACCT	2330
Qy	1250	ACGTTACTGCGGAAGCGCTTGGATAAGCGCGGTGTGCTTGTGCTATATGTTATTTT	1309	Qy	1804	-----	1803
Db	1251	ACGTTACTGCGGAAGCGCTTGGATAAGCGCGGTGTGCTTGTGCTATATGTTATTTT	1310	Db	2331	GGGGGGCAGACACCGCGCGGTGTGGGACATCATCTTGGGCTGCGCGTCTCCGCCGCA	2390
Qy	1310	CCACCATATTCGCGTCTTTTGGCAATGTAGGGCCGGGAACTGGCCCTGTCTTCTGA	1369	Qy	1804	-----	1803
Db	1311	CCACCATATTCGCGTCTTTTGGCAATGTAGGGCCGGGAACTGGCCCTGTCTTCTGA	1370	Db	2391	GGGGGAGGAGATACATCTGGGACCGCGACAGACCTTGAAGGCGAGGGGTGGCGACTCC	2450
Qy	1370	CGAGCATTCCTAGGGGTCTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTGAATGTG	1429	Qy	1804	--CGGCTATATCAGGCTACTCCCAACAGACGAGCGGCTTCTTGGCTGATCATCACTA	1861
Db	1371	CGAGCATTCCTAGGGGTCTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTGAATGTG	1430	Db	2451	TCGCGGCTATATCAGGCTACTCCCAACAGACGAGGCTCTTGGCTGATCATCACTA	2510
Qy	1430	TGAAGGACAGATTCCTCTGAGAGCTTCTTGAAGACAAACAGTCTGTAGCGACCTTT	1489	Qy	1862	GCCTCACAGCCCGGACAGGAACAGGTCTCAGGGGGAGGTCCAAGTGGTCTCCACCGCAA	1921
Db	1431	TGAAGGACAGATTCCTCTGAGAGCTTCTTGAAGACAAACAGTCTGTAGCGACCTTT	1490	Db	2511	GCCTCACAGCCCGGACAGGAACAGGTCTCAGGGGGAGGTCCAAGTGGTCTCCACCGCAA	2570
Qy	1490	GCAGGACGGCAACCCCGACCTGGCAGAGTCCCTCTCGGCCAAAGCCACGCTAT	1549	Qy	1922	CACAAATTTTCTGGCGACCTTGGTCTAATGGCGTGTGTGGACTGTCTATCATGGTCCG	1981
Db	1491	GCAGGACGGCAACCCCGACCTGGCAGAGTCCCTCTCGGCCAAAGCCACGCTAT	1550	Db	2571	CACAAATTTTCTGGCGACCTTGGTCTAATGGCGTGTGTGGACTGTCTATCATGGTCCG	2630
Qy	1550	AAGATACACCTGCAAGGGCGGCAACCCCGAGTGCCACGTTGTGAGTTGAGTGTGG	1609	Qy	1982	GCTCAAGAGCCCTTGGCGCCCAAGGGCCCAATCACCCAAATGTACACAAATGTGACCC	2041
Db	1551	AAGATACACCTGCAAGGGCGGCAACCCCGAGTGCCACGTTGTGAGTTGAGTGTGG	1610	Db	2631	GCTCAAGAGCCCTTGGCGCCCAAGGGCCCAATCACCCAAATGTACACAAATGTGACCC	2690
Qy	1610	AAAGAGTCAATGGCTCTCTCAAGCGTATTCACAGGGGCTGAAGGATGCCAGAGG	1669	Qy	2042	AGGACCTCTGTCGGTGGCAAGCGCCCCCGGGCGGCTTCTTGACACCATGCACTTGG	2101
Db	1611	AAAGAGTCAATGGCTCTCTCAAGCGTATTCACAGGGGCTGAAGGATGCCAGAGG	1670	Db	2691	AGGACCTCTGTCGGTGGCAAGCGCCCCCGGGCGGCTTCTTGACACCATGCACTTGG	2750
Qy	1670	TACCCCATTTATGGGATCTGATCTGGGGCTCGGTCACATGCTTTACATGTGTTAGT	1729	Qy	2102	GCAGCTCGGACCTTTTACTTGGTCAAGGATGCGCGATGTCAATTCGGTGGCGCGGG	2161
Db	1671	TACCCCATTTATGGGATCTGATCTGGGGCTCGGTCACATGCTTTACATGTGTTAGT	1730	Db	2751	GCAGCTCGGACCTTTTACTTGGTCAAGGATGCGCGATGTCAATTCGGTGGCGCGGG	2810
Qy	1730	CGAGGTTAAAAACGCTTAGGCCCCCGAACCAAGGGGACGTGTTTCTTTGAAAAAC	1789	Qy	2162	GGGACAGCGGGGAGGCTACTCTCCCGCAGGGCCGCTCTCTACTTGAAGGGCTCTTCGG	2221
Db	1731	CGAGGTTAAAAACGCTTAGGCCCCCGAACCAAGGGGACGTGTTTCTTTGAAAAAC	1790	Db	2811	GGGACAGCGGGGAGGCTACTCTCCCGCAGGGCCGCTCTCTACTTGAAGGGCTCTTCGG	2870
Qy	1790	ACGATAATACCATG-----	1803	Qy	2222	GGGTCCCACTGCTCTGCGCCCTCGGGGACGCTGTGGGCACTTTTCGGGCTGCCGTGCA	2281
Db	1791	ACGATAATACCATG-----	1850	Db	2871	GGGTCCCACTGCTCTGCGCCCTCGGGGACGCTGTGGGCACTTTTCGGGCTGCCGTGCA	2930
Qy	1804	-----	1803	Qy	2282	CCGAGGGGTTGCGAAGCGGTGACATTTGTACCGCTCGAGTCTATGGAACCACTATGC	2341
Db	1851	TGATACTCTTGACCTTGTACCGGACTATAGCTGTTCTCGCTAGGCTCATATGGTGT	1910	Db	2931	CCGAGGGGTTGCGAAGCGGTGACATTTGTACCGCTCGAGTCTATGGAACCACTATGC	2990
Qy	1804	-----	1803	Qy	2342	GGTCCCGGTTCTTCAAGGACAACTCTGTCCTCCCGCGGTACCGCAGACATTCAGGTGG	2401

QY 2402 CCCATCTACGCCCTTACTGTTAGCGGCAAGACACTAAGGTGCGGCTCGGTATGCAG 2461  
DB 3051 CCCATCTACGCCCTTACTGTTAGCGGCAAGACACTAAGGTGCGGCTCGGTATGCAG 3110  
QY 2462 CCCAAGGGTATTAAGGTGCTTGTCTGTAACCCCTCGTGGCCGCCACCCCTAGTGTTCGGGG 2521  
DB 3111 CCCAAGGGTATTAAGGTGCTTGTCTGTAACCCCTCGTGGCCGCCACCCCTAGTGTTCGGGG 3170  
QY 2522 CGTATATGCTTAAGGACATGTTATCGACCTTAAATCATCAGAACCGGGTAAAGGACATCA 2581  
DB 3171 CGTATATGCTTAAGGACATGTTATCGACCTTAAATCATCAGAACCGGGTAAAGGACATCA 3230  
QY 2582 CCACGGGTGCCCCCATCACTACTCCACTATGCGCAAGTTTCTTCCGCAAGGTGCTTGTCT 2641  
DB 3231 CCACGGGTGCCCCCATCACTACTCCACTATGCGCAAGTTTCTTCCGCAAGGTGCTTGTCT 3290  
QY 2642 CTGGGGGGCCCTATGACATCATATATATGATGAGTGCCACTCAACTGACTCGACACTA 2701  
DB 3291 CTGGGGGGCCCTATGACATCATATATATGATGAGTGCCACTCAACTGACTCGACACTA 3350  
QY 2702 TCCTGGGATCGGCACAGTCTGAGGACCAAGCGGAGACGGCTGGAGGGGACTCGTCTGTC 2761  
DB 3351 TCCTGGGATCGGCACAGTCTGAGGACCAAGCGGAGACGGCTGGAGGGGACTCGTCTGTC 3410  
QY 2762 TCGCCACCGCTACGCTCCGGGATCGGTCAACCGTGCCACATCCAAACATCGAGGAGGTGG 2821  
DB 3411 TCGCCACCGCTACGCTCCGGGATCGGTCAACCGTGCCACATCCAAACATCGAGGAGGTGG 3470  
QY 2822 CTGTCTCAGCACTGGAGAAATCCCTTTATGCGCAAGCCATCCCATTCGAGACCATCA 2881  
DB 3471 CTGTCTCAGCACTGGAGAAATCCCTTTATGCGCAAGCCATCCCATTCGAGACCATCA 3530  
QY 2882 AGGGGGGAGGACCTCATTTCTGCCATTCGCAAGAAATGCTATGACTCGCGCGGA 2941  
DB 3531 AGGGGGGAGGACCTCATTTCTGCCATTCGCAAGAAATGCTATGACTCGCGCGGA 3590  
QY 2942 AGCTGTCCGGGCTCGGACTCAATGCTGATGATATTAACGGGGGCTTGTATGATCCGTCA 3001  
DB 3591 AGCTGTCCGGGCTCGGACTCAATGCTGATGATATTAACGGGGGCTTGTATGATCCGTCA 3650  
QY 3002 TACCAACTAGGGAGACGTCTATGCTGAGCAACCGGACGCTCTAATGACGGGCTTTACCG 3061  
DB 3651 TACCAACTAGGGAGACGTCTATGCTGAGCAACCGGACGCTCTAATGACGGGCTTTACCG 3710  
QY 3062 GCGATTTGCACTCAGTGATCGACTGCAATATATGCTGATGATATTAACGGGGGCTTGTATGATCCGTCA 3121  
DB 3711 GCGATTTGCACTCAGTGATCGACTGCAATATATGCTGATGATATTAACGGGGGCTTGTATGATCCGTCA 3770  
QY 3122 TGGACCCGACCTTCAACATTTGAGACGACGACCGGTGCCCAAGACGCGGTGTCAAGCTCGC 3181  
DB 3771 TGGACCCGACCTTCAACATTTGAGACGACGACCGGTGCCCAAGACGCGGTGTCAAGCTCGC 3830  
QY 3182 AGCGGCGAGGACGACTGTTAGGGGACGAGATGGGCATTTAAGGTTTGTGACTCGAGGAG 3241  
DB 3831 AGCGGCGAGGACGACTGTTAGGGGACGAGATGGGCATTTAAGGTTTGTGACTCGAGGAG 3890  
QY 3242 AACGGCCCTCGGGATGTTGATTTCTCGTCTGCTGCGAGTGTCTATCAGCGGGGCTGTG 3301  
DB 3891 AACGGCCCTCGGGATGTTGATTTCTCGTCTGCTGCGAGTGTCTATCAGCGGGGCTGTG 3950  
QY 3302 CTTGGTACGAGCTCAGCGCCCGGACGACTCAGTTTGTGGGCTTACCTTAAACACAC 3361  
DB 3951 CTTGGTACGAGCTCAGCGCCCGGACGACTCAGTTTGTGGGCTTACCTTAAACACAC 4010  
QY 3362 CAGGGTTGCCGTCTGCGAGGACCATATGAGGATCTGGGAGAGCGTCTTTTACAGGCTCA 3421  
DB 4011 CAGGGTTGCCGTCTGCGAGGACCATATGAGGATCTGGGAGAGCGTCTTTTACAGGCTCA 4070  
QY 3422 CCCACATAGACCCCATTTCTTGTGTCGAGCTATGAGGAGGAGGACAACTTCCCTTACC 3481  
DB 4071 CCCACATAGACCCCATTTCTTGTGTCGAGCTATGAGGAGGAGGACAACTTCCCTTACC 4130

QY 3482 TGGTAGCATACACAGGCTACGGTGTGCGCACAGGGCTCAGGCTCCAGCTCCATCGTGGGACC 3541  
DB 4131 TGGTAGCATACACAGGCTACGGTGTGCGCACAGGGCTCAGGCTCCAGCTCCATCGTGGGACC 4190  
QY 3542 AAATGTGAAGTGTCTCATACGGCTTAAAGCCCTACGCTGCACGGGCAACCGCCCTGCTGT 3601  
DB 4191 AAATGTGAAGTGTCTCATACGGCTTAAAGCCCTACGCTGCACGGGCAACCGCCCTGCTGT 4250  
QY 3602 ATAGCTGGGAGCGCTTCAAAACGAGGTATACACACACACCCCATAAACAAATACATCA 3661  
DB 4251 ATAGCTGGGAGCGCTTCAAAACGAGGTATACACACACACCCCATAAACAAATACATCA 4310  
QY 3662 TGGCATGATGTCGGCTGACCTGGAGGTGCTCAACAGACACCTGGTGTGCTGGTAGCGGAG 3721  
DB 4311 TGGCATGATGTCGGCTGACCTGGAGGTGCTCAACAGACACCTGGTGTGCTGGTAGCGGAG 4370  
QY 3722 TCCTAGAGCTCTGCGCCGCTATTGSCCTGACAAAGGAGCGTGTGCTATGTTGGGACGGA 3781  
DB 4371 TCCTAGAGCTCTGCGCCGCTATTGSCCTGACAAAGGAGCGTGTGCTATGTTGGGACGGA 4430  
QY 3782 TCATCTTGTCCGGAAGCGGCGCATATTCCGACAGGGAAGTCTTTTACCGGGAGTTCCG 3841  
DB 4431 TCATCTTGTCCGGAAGCGGCGCATATTCCGACAGGGAAGTCTTTTACCGGGAGTTCCG 4490  
QY 3842 ATGAGATGGAAGAGTGGCCCTCACACCTCCCTTACATCGAACAGGGAATGACAGCTCGCG 3901  
DB 4491 ATGAGATGGAAGAGTGGCCCTCACACCTCCCTTACATCGAACAGGGAATGACAGCTCGCG 4550  
QY 3902 AACAAATTCAGGAGCAATCGGTTGCTGCAAAAGCCACCAAGCAAGCGGAGGCTG 3961  
DB 4551 AACAAATTCAGGAGCAATCGGTTGCTGCAAAAGCCACCAAGCAAGCGGAGGCTG 4610  
QY 3962 CTGCTCCGCTGGTGAATCAGTGGGAGCGCTCGAAGCCTTCTGGGCGAAGCATATGT 4021  
DB 4611 CTGCTCCGCTGGTGAATCAGTGGGAGCGCTCGAAGCCTTCTGGGCGAAGCATATGT 4670  
QY 4022 GGAATTTTCATCAGCGGATACAAATATTTAGCAGGCTTGTCCACTCTGCTGSCAACCCCG 4081  
DB 4671 GGAATTTTCATCAGCGGATACAAATATTTAGCAGGCTTGTCCACTCTGCTGSCAACCCCG 4730  
QY 4082 CGATAGCATCACTGATGGCATTCACAGCTCTATCACCAGCCGCTCACACCCCAACATA 4141  
DB 4731 CGATAGCATCACTGATGGCATTCACAGCTCTATCACCAGCCGCTCACACCCCAACATA 4790  
QY 4142 CCCTCTGTTTAAACATCTGCGGGGATGGGTGGCGGCCAACTTGTCTCTCCACGCGCTG 4201  
DB 4791 CCCTCTGTTTAAACATCTGCGGGGATGGGTGGCGGCCAACTTGTCTCTCCACGCGCTG 4850  
QY 4202 CTTCTGCTTTCGTAGGCGCGGATCGCTGAGCGGCTGTTGGCAGCATAGGCTTGGGA 4261  
DB 4851 CTTCTGCTTTCGTAGGCGCGGATCGCTGAGCGGCTGTTGGCAGCATAGGCTTGGGA 4910  
QY 4262 AGGTGCTTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGGCTCGTGGGCT 4321  
DB 4911 AGGTGCTTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGGCTCGTGGGCT 4970  
QY 4322 TTAAGTCAATGAGCGGCGGATGCCCTCCACGAGGACCTGGTTAACTACTCCCTGCTA 4381  
DB 4971 TTAAGTCAATGAGCGGCGGATGCCCTCCACGAGGACCTGGTTAACTACTCCCTGCTA 5030  
QY 4382 TCCTCTCCCTTGGCGGCTTGTGCTGCGGGTGTGCGCAGCATACTGCTGGGACG 4441  
DB 5031 TCCTCTCCCTTGGCGGCTTGTGCTGCGGGTGTGCGCAGCATACTGCTGGGACG 5090  
QY 4442 TGGGCCCAAGGGGAGGGGCTGTGAGTGGATGAACCGGCTGATAGCGTTCCCTTCGCGG 4501  
DB 5091 TGGGCCCAAGGGGAGGGGCTGTGAGTGGATGAACCGGCTGATAGCGTTCCCTTCGCGG 5150  
QY 4502 GTAAACAGTCTCCCGCAGCAGCATATGCTGCTGAGAGCAGCGTGCAGCAGTGTCACTC 4561  
DB 5151 GTAAACAGTCTCCCGCAGCAGCATATGCTGCTGAGAGCAGCGTGCAGCAGTGTCACTC 5210  
QY 4562 AGATCTCTCTAGTCTTTACCATCACTCAGCTGCTGTAAGAGGCTTCAACGAGTGATCAACG 4621

5211	Db		AGATCCCTCTCTAGTCTTACCATCACTCAGCTGCTGAAAGAGGCTTCCACAGTGAATCAACG	5270
4622	Qy		AGGACTGCTCCACGCCATGCTCGGCTCGTGGCTAAGAGATGTTTGGATATGCA	4681
5271	Db		AGGACTGCTCCACGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGATATGCA	5330
4682	Qy		CGGTGTTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGCTCCTGCCCGCATTTGCCGGAG	4741
5331	Db		CGGTGTTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGCTCCTGCCCGCATTTGCCGGAG	5390
4742	Qy		TCCCTCTTCTCATGTCAACGTGGGTACAAAGGAGTCTGGCGGGGCGACGGCATATGC	4801
5391	Db		TCCCTCTTCTCATGTCAACGTGGGTACAAAGGAGTCTGGCGGGGCGACGGCATATGC	5450
4802	Qy		AAACCACTGCCCATGTGGACACAGATCACCGACATGTGAAAAAGGTTCCATAGGA	4861
5451	Db		AAACCACTGCCCATGTGGACACAGATCACCGACATGTGAAAAAGGTTCCATAGGA	5510
4862	Qy		TCGTGGGCTTAGGACCTGTAGTAACACGTGGCATGGAACAATTTCCCAATTAACGCGTACA	4921
5511	Db		TCGTGGGCTTAGGACCTGTAGTAACACGTGGCATGGAACAATTTCCCAATTAACGCGTACA	5570
4922	Qy		CCACGGGCCCTGACGCCCTTCCCGCGCGCAAAATTAATTCAGGGGCGTGTGGGGGTGG	4981
5571	Db		CCACGGGCCCTGACGCCCTTCCCGCGCGCAAAATTAATTCAGGGGCGTGTGGGGGTGG	5630
4982	Qy		CTGCTGAGGAGTACGTGGAGTTACGGGGTGGGGATTTCCACTAGTGACGGGCATGA	5041
5631	Db		CTGCTGAGGAGTACGTGGAGTTACGGGGTGGGGATTTCCACTAGTGACGGGCATGA	5690
5042	Qy		CCACTGACAAAGTAAAGTCCCGTGTGAGTTCCGGCCCCCGAAATTTTTCACAGAAGTGG	5101
5691	Db		CCACTGACAAAGTAAAGTCCCGTGTGAGTTCCGGCCCCCGAAATTTTTCACAGAAGTGG	5750
5102	Qy		ATGGGCTGCGGTTGCACAGGTACGCTCCAGCGTCCAAACCCCTCTCTACGGGAGGAGTCA	5161
5751	Db		ATGGGCTGCGGTTGCACAGGTACGCTCCAGCGTCCAAACCCCTCTCTACGGGAGGAGTCA	5810
5162	Qy		CATTCTGCTGGGCTCAATCAATACTGGTTGGGTACAGCTCCCATGCGAGCCGCAAC	5221
5811	Db		CATTCTGCTGGGCTCAATCAATACTGGTTGGGTACAGCTCCCATGCGAGCCGCAAC	5870
5222	Qy		CGGAGTACAGTGTCACTTCCATGTCCAGCACCCCTCCACATACGGCGGAGACGG	5281
5871	Db		CGGAGTACAGTGTCACTTCCATGTCCAGCACCCCTCCACATACGGCGGAGACGG	5930
5282	Qy		CTAAGCGTAGGCTGGCCAGGGGATCTCCGCCCTCTTGGCCAGCTCATAGTACGCCAGC	5341
5931	Db		CTAAGCGTAGGCTGGCCAGGGGATCTCCGCCCTCTTGGCCAGCTCATAGTACGCCAGC	5990
5342	Qy		TGCTGCGGCTTCTTGAAGGCAATGCACTACCCGTCATGATCTCCCGGAGCGTGACC	5401
5991	Db		TGCTGCGGCTTCTTGAAGGCAATGCACTACCCGTCATGATCTCCCGGAGCGTGACC	6050
5402	Qy		TCATCGAGGCCAACTCTGTCGGCGGAGAGATGGCGGAAATCAACCCCGTGGAGT	5461
6051	Db		TCATCGAGGCCAACTCTGTCGGCGGAGAGATGGCGGAAATCAACCCCGTGGAGT	6110
5462	Qy		CAGAAAAAAGGTAGTAAATTTTGGACTCTTTTCGAGCGGCTCCAAAGCGGAGGAGTGA	5521
6111	Db		CAGAAAAAAGGTAGTAAATTTTGGACTCTTTTCGAGCGGCTCCAAAGCGGAGGAGTGA	6170
5522	Qy		GGGAAGTATCGTTCCGGCGGAGATCTCGGAGGTTCAGAAATTTCCCTCGAGGATGC	5581
6171	Db		GGGAAGTATCGTTCCGGCGGAGATCTCGGAGGTTCAGAAATTTCCCTCGAGGATGC	6230
5582	Qy		CCATATGGCGACCGCGGATTTACACCTTCCACTGTTAGAGTCTTGGGAAGCACCGGACT	5641
6231	Db		CCATATGGCGACCGCGGATTTACACCTTCCACTGTTAGAGTCTTGGGAAGCACCGGACT	6290
5642	Qy		ACGTCCCTCCAGTGTACAGGGGTGTCCATTTGCCGCTTCCCAAGGCGCCCTCCGATACCAC	5701



QY	481	CTGATCCCGCGCTGTTCGGCTGTTCAGCGAGGGCGCCCGTCTTTTGTCAAGACG	540	Db	1550	TAAGATACACCTGCAAGGCGGCAACACCCAGTCCACGTTGTGAGTTGATGTTGTG	1609
Db	481	CTGATCCCGCGCTGTTCGGCTGTTCAGCGAGGGCGCCCGTCTTTTGTCAAGACG	540	QY	1609	GAAGAGTCAAAATGGCTCTCCTCAAGCGTATTCAACAAGGGCTGAAGGATGCCAAG	1668
QY	541	ACCTGTCCGGTCCCTGAATGAATGCACTCAGAGACGAGGCGGGCTATCGTGGCTGGCA	600	Db	1610	GAAGAGTCAAAATGGCTCTCCTCAAGCGTATTCAACAAGGGCTGAAGGATGCCAAG	1669
Db	541	ACCTGTCCGGTCCCTGAATGAATGCACTCAGAGACGAGGCGGGCTATCGTGGCTGGCA	600	QY	1669	GTACCCCATTTGATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTGTTAG	1728
QY	601	CGACGGCGCTTCTTTCGCGAGCTGTCTCGACTGTGTCTACTGAAGCGGAAGGACTGCG	660	Db	1670	GTACCCCATTTGATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTGTTAG	1729
Db	601	CGACGGCGCTTCTTTCGCGAGCTGTCTCGACTGTGTCTACTGAAGCGGAAGGACTGCG	660	QY	1729	TCGAGTTTAAAAAGTCTAGGCCCGCCGAAACCAACGAGGACGTGGTTTCTTTGAAAA	1788
QY	661	TGCTATTGGCGAAGTGCCTGGGCGAGATCTCTGTCTCTCACTCTGCTGCGGAGA	720	Db	1730	TCGAGTTTAAAAAGTCTAGGCCCGCCGAAACCAACGAGGACGTGGTTTCTTTGAAAA	1789
Db	661	TGCTATTGGCGAAGTGCCTGGGCGAGATCTCTGTCTCTCACTCTGCTGCGGAGA	720	QY	1789	CACGATAATACCATG-----	1803
QY	721	AGTATCCATCATGGCTGATGCAATGCGCGGCTGCATACGCTTGATCCGGCTACTGCG	780	Db	1790	CACGATAATACCATGCAACGGGAGATGGCAGCATCGTGGGAGGCGGGTTTTTCGTAGGT	1849
Db	721	AGTATCCATCATGGCTGATGCAATGCGCGGCTGCATACGCTTGATCCGGCTACTGCG	780	QY	1804	-----	1803
QY	781	CATTTCGACCACCAAGCGAAACATCGCATCGAGCGACGCTACTCGGATGGAAGCGGTC	840	Db	1850	CTGATACTCTTGACCTTGTCACCGCATATAAGCTGTTCTCGTAGGCTCATATGGTGG	1909
Db	781	CATTTCGACCACCAAGCGAAACATCGCATCGAGCGACGCTACTCGGATGGAAGCGGTC	840	QY	1804	-----	1803
QY	841	TTGTGATCAGGATGATCTGAGCAAGAGACATCAGGGGCTCGCGCAGCGAACTGTTGG	900	Db	1910	TTACAATATTTTATCACCAGGCGGAGGACACATTGCAAGTGTGGATCCCCCCTCAAC	1969
Db	841	TTGTGATCAGGATGATCTGAGCAAGAGACATCAGGGGCTCGCGCAGCGAACTGTTGG	900	QY	1804	-----	1803
QY	901	CCAGGCTCAGGCGGCGATGCGCGAGGAGATCTCGTGTGACCCATGCGATGCGCT	960	Db	1970	GTTCGGGGGCGCGATGCCGTCATCTCTCCTCAGCTGCGCGATCCACCCAGAGCTAATC	2029
Db	901	CCAGGCTCAGGCGGCGATGCGCGAGGAGATCTCGTGTGACCCATGCGATGCGCT	960	QY	1804	-----	1803
QY	961	GCTTCCGGAATCATGTGTGAAATGCGCGCTTTTCTGGATTCATGAGTCTGGCGGC	1020	Db	2030	TTTACCATCACCATAATCTTGCTCGCCATACTCGGTCCACTCATGTGTGCTCCAGGTGCT	2089
Db	961	GCTTCCGGAATCATGTGTGAAATGCGCGCTTTTCTGGATTCATGAGTCTGGCGGC	1020	QY	1804	-----	1803
QY	1021	TGGGTGTGGCGACCGCTATCAGGACATAGCGTTGGCTACCGGTGATTTGCTGAAGAGC	1080	Db	2090	ATAACAAAGTCCGTACTTCTGTGCGCGCACACGGGCTCAITTCGTGCAATGCAATGCTGGTG	2149
Db	1021	TGGGTGTGGCGACCGCTATCAGGACATAGCGTTGGCTACCGGTGATTTGCTGAAGAGC	1080	QY	1804	-----	1803
QY	1081	TTGGCGGCAATGGGCTGACCGCTCTCGTCTTACGGTATCGCGCTCCCGATTGCG	1140	Db	2150	CGAAGTTGTGGGGTCAITATGTCCAAATGGCTCTCATGAAATGCTGCGCAGCTGACA	2209
Db	1081	TTGGCGGCAATGGGCTGACCGCTCTCGTCTTACGGTATCGCGCTCCCGATTGCG	1140	QY	1804	-----	1803
QY	1141	AGCGCATCGCTTCTATCGCTTCTTGAAGTCTTCTGAGTT-----TAAA	1188	Db	2210	GGTACGTACTTTATGACCATCTCACCCACTGCGGACTGGGCCACCGGGGCTTACGA	2269
Db	1141	AGCGCATCGCTTCTATCGCTTCTTGAAGTCTTCTGAGTT-----TAAA	1200	QY	1804	-----	1803
QY	1189	CAGACCAACCGTTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTCT	1248	Db	2270	GACCTTGGGTGGCAGTTGAGCCCTGCTTCTCTGATATGGAGACCAAGGTTATCAC	2329
Db	1201	CAGACCAACCGTTTCCCTCTAGCGGATCAATTCGCG-----CCCGCCCTCT	1249	QY	1804	-----	1803
QY	1249	AAAGTTACTGGCGGAGCGCTTGGAAATAGCGCGGTGCGTGTGCTATATGTTATTT	1308	Db	2330	TGGGGGCGAGACACCGCGGCTGTGGGGACATCATCTTGGGCTGCCCTCTCCGCCCGC	2389
Db	1250	AAAGTTACTGGCGGAGCGCTTGGAAATAGCGCGGTGCGTGTGCTATATGTTATTT	1309	QY	1804	-----	1803
QY	1309	TCCACCATATGCGCTTCTTGGCAATGTAGGGCGCGGAAACCTGGCCCTGTCTTCTTG	1368	Db	2390	AGGGGAGGAGATACATCTGGGACCGGACAGAGCCTTTGAAGGCGAGGGTGGCGACTC	2449
Db	1310	TCCACCATATGCGCTTCTTGGCAATGTAGGGCGCGGAAACCTGGCCCTGTCTTCTTG	1369	QY	1804	---GCGCTTATTCGCGCTACTCCCAACAGACGAGGCGCTACTTGGCTGCATCATCACT	1860
QY	1369	ACGAGATTCCTAGGGGTCTTCCCTCTCGCCCAAGAGGATGCAAGGTCTGTTGAATGTC	1428	Db	2450	CTCGCGCTTATTCGCGCTACTCCCAACAGACGCGAGGCGCTACTTGGCTGCATCATCACT	2509
Db	1370	ACGAGATTCCTAGGGGTCTTCCCTCTCGCCCAAGAGGATGCAAGGTCTGTTGAATGTC	1429	QY	1861	AGCCTCACAGGCGGAGACAGGAACACAGGTTCGAGGGGAGGTCCAAGTGTCTCCACCGCA	1920
QY	1429	GTGAAGGAAGAGTCTCTCTGGAAGTCTCTTGAAGACAAACACGCTGTAGCGACCTTT	1488	Db	2510	AGCCTCACAGGCGGAGACAGGAACACAGGTTCGAGGGGAGGTCCAAGTGTCTCCACCGCA	2569
Db	1430	GTGAAGGAAGAGTCTCTCTGGAAGTCTCTTGAAGACAAACACGCTGTAGCGACCTTT	1489	QY	1921	ACAAATCTTCTCGCGACCTGCGTCAATGGCGTGTGTGAGCTGTCTATCATGTGTC	1980
QY	1489	TGCAGGACGGAACCCCGACCTGCGGACAGGTGCTCTGCGGCCAAAAGCACCTGTA	1548	Db	2570	ACAAATCTTCTCGCGACCTGCGTCAATGGCGTGTGTGAGCTGTCTATCATGTGTC	2629
Db	1490	TGCAGGACGGAACCCCGACCTGCGGACAGGTGCTCTGCGGCCAAAAGCACCTGTA	1549	QY	1981	GGCTCAAGACCTTTCGCGGCCAAAGGGCCCAATCACCACCAATGTACACCAATGTGGAC	2040
QY	1549	TAAGATACACCTGCAAGGGCGGACAAACCCAGTGCCAGTTGTGATGTTGTG	1608				

Db 2630 GGCTCAAAGACCTTGGCCGGCCAAAGGGCCCAAATCACCAAAATGTACCAATGTGGAC 2689  
 Qy 2041 CAGGACCTCGTGGCTGGCAAGCGCCCCCGGGCGCGTTCCTTTGACACCATGCACTCGC 2100  
 Db 2690 CAGGACCTCGTGGCTGGCAAGCGCCCCCGGGCGCGTTCCTTTGACACCATGCACTCGC 2749  
 Qy 2101 GGCAGCTCGGACCTTTACTTTGGTACGAGGCAATGCGATGTCAATTCGCGTGGCGGGG 2160  
 Db 2750 GGCAGCTCGGACCTTTACTTTGGTACGAGGCAATGCGATGTCAATTCGCGTGGCGGGG 2809  
 Qy 2161 GGCACAGAGGGGAGGACCTACTCTCCCGCCAGCGCGCTCTCTACTTTGAGGGCTCTTCG 2220  
 Db 2810 GGCACAGAGGGGAGGACCTACTCTCCCGCCAGCGCGCTCTCTACTTTGAGGGCTCTTCG 2869  
 Qy 2221 GCGGTGCCACTCTCTCGCCCTCGGGGCAAGCTGTGGGCAATCTTTCCGGCTCGCGGTGC 2280  
 Db 2870 GCGGTGCCACTCTCTCGCCCTCGGGGCAAGCTGTGGGCAATCTTTCCGGCTCGCGGTGC 2929  
 Qy 2281 ACCCGAGGGGTTCGAAAGCGGTGGAATTTGTACCCGTGCGAGTCTATGGAACCACTATG 2340  
 Db 2930 ACCCGAGGGGTTCGAAAGCGGTGGAATTTGTACCCGTGCGAGTCTATGGAACCACTATG 2989  
 Qy 2341 CCGTCCCGGTCTTCAAGGCAAACTCGTCCCTCCGGCGGTACCGGCAATTCAGGTG 2400  
 Db 2990 CCGTCCCGGTCTTCAAGGCAAACTCGTCCCTCCGGCGGTACCGGCAATTCAGGTG 3049  
 Qy 2401 GCCCATCTACAGCCCTTACTGTAGCGGCAAGAGCACTAAGGTGCGGCTGCGTATGCA 2460  
 Db 3050 GCCCATCTACAGCCCTTACTGTAGCGGCAAGAGCACTAAGGTGCGGCTGCGTATGCA 3109  
 Qy 2461 GCCCAAGGGTAAAGTCTGTCTCTGAACCGGTCCGTCGCGGCAATTCAGGTG 2520  
 Db 3110 GCCCAAGGGTAAAGTCTGTCTCTGAACCGGTCCGTCGCGGCAATTCAGGTG 3169  
 Qy 2521 CGGTATATGTCTAAGGCAATGTATCGACCTACATCAAGGCAAGAGCACTAAGGTGCGGCTGCGTATGCA 2580  
 Db 3170 CGGTATATGTCTAAGGCAATGTATCGACCTACATCAAGGCAAGAGCACTAAGGTGCGGCTGCGTATGCA 3229  
 Qy 2581 ACCAGGGTGCCTCATCACCTACTTCCACCTATGGCAAGTTCCTTCCGCAAGCTGCTGCTG 2640  
 Db 3230 ACCAGGGTGCCTCATCACCTACTTCCACCTATGGCAAGTTCCTTCCGCAAGCTGCTGCTG 3289  
 Qy 2641 TCTGGGGCGCTATGACATCATATATGTGATGATGCCCTCAATCTGATCGACCACT 2700  
 Db 3290 TCTGGGGCGCTATGACATCATATATGTGATGATGCCCTCAATCTGATCGACCACT 3349  
 Qy 2701 ATCTCTGGGCATCGGCACAGTCTCTGGAACCAAGGAGCGGTGAGCGCGACTCGTCTG 2760  
 Db 3350 ATCTCTGGGCATCGGCACAGTCTCTGGAACCAAGGAGCGGTGAGCGCGACTCGTCTG 3409  
 Qy 2761 CTCGCCACCGCTACGCTCCGGATCGGTCAACCTGCGCAATCCAAACATCGAGAGGTG 2820  
 Db 3410 CTCGCCACCGCTACGCTCCGGATCGGTCAACCTGCGCAATCCAAACATCGAGAGGTG 3469  
 Qy 2821 GCTCTGCGACCTGGAAGTATCCCTTTTATGGCAAGCCATCCCATCGAGACCACT 2880  
 Db 3470 GCTCTGCGACCTGGAAGTATCCCTTTTATGGCAAGCCATCCCATCGAGACCACT 3529  
 Qy 2881 AAGGGGGGAGGACCTCATTTCTGCGATTCGAAGAGAAATGTGATGAGCTCGCGCG 2940  
 Db 3530 AAGGGGGGAGGACCTCATTTCTGCGATTCGAAGAGAAATGTGATGAGCTCGCGCG 3589  
 Qy 2941 AAGCTGTCGGCTCGGACCTCAATGCTGTAGCAATATACCGGGGCTTGTATGATCGCTC 3000  
 Db 3590 AAGCTGTCGGCTCGGACCTCAATGCTGTAGCAATATACCGGGGCTTGTATGATCGCTC 3649  
 Qy 3001 ATACCAACTAGCGAGAGCTGATGCTAGCAAGCGGCTCTAATGACGGGCTTTACC 3060  
 Db 3650 ATACCAACTAGCGAGAGCTGATGCTAGCAAGCGGCTCTAATGACGGGCTTTACC 3709  
 Qy 3061 GGCATTTCCAGTCTGAGTCTGCAATATGCTGTCACCCAGACAGTCTGCTCAGC 3120  
 Db 3710 GGCATTTCCAGTCTGAGTCTGCAATATGCTGTCACCCAGACAGTCTGCTCAGC 3769

Qy 3121 CTGGACCCGACCTTCAACATTTGAGACGAGCAAGGTGCCACAAGACGCGGTGTACGCTCG 3180  
 Db 3770 CTGGACCCGACCTTCAACATTTGAGACGAGCAAGGTGCCACAAGACGCGGTGTACGCTCG 3829  
 Qy 3181 CAGCGCGAGGCGAGGACCTGGTATGGGCGAGGATGGGCAATTTACAGGTTTCTGACTCCAGGA 3240  
 Db 3830 CAGCGCGAGGCGAGGACCTGGTATGGGCGAGGATGGGCAATTTACAGTCTTGTGACTCCAGGA 3889  
 Qy 3241 GAAACGCGCTCGGCGATGTTTCAATTTCTCGTTCCTGAGTGTATGACGCGGCTGT 3300  
 Db 3890 GAAACGCGCTCGGCGATGTTTCAATTTCTCGTTCCTGAGTGTATGACGCGGCTGT 3949  
 Qy 3301 GCTTGTGACGAGCTCACGCGCGGAGACCTCAGTTAGTTCGCGGCTTACCTAACAACA 3360  
 Db 3950 GCTTGTGACGAGCTCACGCGCGGAGACCTCAGTTAGTTCGCGGCTTACCTAACAACA 4009  
 Qy 3361 CCAGGTTGCCGCTCTGCGAGGACCATCTGGAGTTCTGGGAGAGCTCTTTACAGGCTTC 3420  
 Db 4010 CCAGGTTGCCGCTCTGCGAGGACCATCTGGAGTTCTGGGAGAGCTCTTTACAGGCTTC 4069  
 Qy 3421 ACCCATAGAGCGCCATTTCTTGTCCAGACTAAGCAGGCGAGGAGACAATTTCCCTTAC 3480  
 Db 4070 ACCCATAGAGCGCCATTTCTTGTCCAGACTAAGCAGGCGAGGAGACAATTTCCCTTAC 4129  
 Qy 3481 CTGGTAGCATACAGGCTACGCGTACGCGGCTCAGGCTCAGGCTCCACCTCCATCGTGGAC 3540  
 Db 4130 CTGGTAGCATACAGGCTACGCGTACGCGGCTCAGGCTCAGGCTCCACCTCCATCGTGGAC 4189  
 Qy 3541 CAATGTGGAAGTGTCTCATACGCTAAAGCTACGCTGACAGGCGCAACGCGCTGCTG 3600  
 Db 4190 CAATGTGGAAGTGTCTCATACGCTAAAGCTACGCTGACAGGCGCAACGCGCTGCTG 4249  
 Qy 3601 TATAGGCTGGAGCGGTTCAAAAGAGGTTACTACCAACACCCCAATACCAATACATC 3660  
 Db 4250 TATAGGCTGGAGCGGTTCAAAAGAGGTTACTACCAACACCCCAATACCAATACATC 4309  
 Qy 3661 ATGGCATCATGTGGCTGACCTGAGGTCTCTGAGGCTCAGGACCTGCTGCTGCTGCTG 3720  
 Db 4310 ATGGCATCATGTGGCTGACCTGAGGTCTCTGAGGCTCAGGACCTGCTGCTGCTGCTG 4369  
 Qy 3721 GTCCTAGCAGCTCTGGCGCGCTATTTGCTGACAAAGGAGGCTGCTGCTGCTGCTGCTG 3780  
 Db 4370 GTCCTAGCAGCTCTGGCGCGCTATTTGCTGACAAAGGAGGTTCTTTTACCGGAGTTC 4429  
 Qy 3781 ATGATCTTCTCGGAAAGCGGCGCTCATTTCCCGAGAGGAGTCTTTTACCGGAGTTC 3840  
 Db 4430 ATGATCTTCTCGGAAAGCGGCGCTCATTTCCCGAGAGGAGTCTTTTACCGGAGTTC 4489  
 Qy 3841 GATGAGATGGAAGAGTGGCGCTCACCTCCCTTACATCGAAAGGAGTCTTTTACCGGAGTTC 3900  
 Db 4490 GATGAGATGGAAGAGTGGCGCTCACCTCCCTTACATCGAAAGGAGTCTTTTACCGGAGTTC 4549  
 Qy 3901 GAACAAATCAACAGAGGCAATCGGTTGCTGCAACAGGAGCAACAGGAGGAGGCT 3960  
 Db 4550 GAACAAATCAACAGAGGCAATCGGTTGCTGCAACAGGAGCAACAGGAGGAGGCT 4609  
 Qy 3961 GCTGCTCCCGTGGTGGATTCAGTGGGAGCCCTCGAAGGCTTCTGGGCGAGCATATG 4020  
 Db 4610 GCTGCTCCCGTGGTGGATTCAGTGGGAGCCCTCGAAGGCTTCTGGGCGAGCATATG 4669  
 Qy 4021 TGGAAATTTCAACAGGAGTACAAATTTTACGAGGCTTGTCCACTCTGCTGCGCAACCCC 4080  
 Db 4670 TGGAAATTTCAACAGGAGTACAAATTTTACGAGGCTTGTCCACTCTGCTGCGCAACCCC 4729  
 Qy 4081 GCGATAGCATCACTGATGGCATTCACAGCTCTTATACACGCGGCTCACCACCAACAT 4140  
 Db 4730 GCGATAGCATCACTGATGGCATTCACAGCTCTTATACACGCGGCTCACCACCAACAT 4789  
 Qy 4141 ACCCTCTGTTTAACTCTCTGGGGAGTGGTGGCGGCCCAACTTGTCTCTCCAGGCT 4200  
 Db 4790 ACCCTCTGTTTAACTCTCTGGGGAGTGGTGGCGGCCCAACTTGTCTCTCCAGGCT 4849



Db	7010	CTGGAAGACACTGAGACACCAATTGACACACCATTATCGGCAAAATAGGTTTTCTGC	7069
Qy	6421	GTCCAAACAGAGAGAGGGGGCGCAAGCAGCTGCGCTTATTCGTATTTCCCAAGATTGGGG	6480
Db	7070	GTCCAAACAGAGAGAGGGGGCGCAAGCAGCTGCGCTTATTCGTATTTCCCAAGATTGGGG	7129
Qy	6481	GTTCTGTGTGTCGAGAAATAGCCCTTTTACGATGTGTCTCCACCCCTCCCTCAGGCCGTG	6540
Db	7130	GTTCTGTGTGTCGAGAAATAGCCCTTTTACGATGTGTCTCCACCCCTCCCTCAGGCCGTG	7189
Qy	6541	ATGGGCTCTTCATACCGATTCCAATACTCTCTCCGACAGCGGGTCAAGTTCCTGCTGAAT	6600
Db	7190	ATGGGCTCTTCATACCGATTCCAATACTCTCTCCGACAGCGGGTCAAGTTCCTGCTGAAT	7249
Qy	6601	GCCTGGAAGCGAAGAAATGCGCTTATGGCTTCGATATGACACCGCGTGTTCGACTCA	6660
Db	7250	GCCTGGAAGCGAAGAAATGCGCTTATGGCTTCGATATGACACCGCGTGTTCGACTCA	7309
Qy	6661	ACGGTCACTGAGATGACATCCGTTGTGAGGAGTCAATCTACCAATGTTGTGACTTGGCC	6720
Db	7310	ACGGTCACTGAGATGACATCCGTTGTGAGGAGTCAATCTACCAATGTTGTGACTTGGCC	7369
Qy	6721	CCCGAAGCAGACAGGGCCATAGGTGCGTCTACAGAGCGGCTTTACATCGGGGGCCCCCTG	6780
Db	7370	CCCGAAGCAGACAGGGCCATAGGTGCGTCTACAGAGCGGCTTTACATCGGGGGCCCCCTG	7429
Qy	6781	ACTAATTTCTAAGGGCAGAACTGCGGCTATCGCGGTGCGCGGCGAGCGGTGTACTGACG	6840
Db	7430	ACTAATTTCTAAGGGCAGAACTGCGGCTATCGCGGTGCGCGGCGAGCGGTGTACTGACG	7489
Qy	6841	ACCAGCTGCGGTATATACCTCACATGTTTACGTTGAAGCGCGTGGCGGCTGTGAGCTGCG	6900
Db	7490	ACCAGCTGCGGTATATACCTCACATGTTTACGTTGAAGCGCGTGGCGGCTGTGAGCTGCG	7549
Qy	6901	AAGCTCCAGGACTCGACGATGCTCGTATGCGGAGACGACCTTGTGTTTATCTGTGAAGC	6960
Db	7550	AAGCTCCAGGACTCGACGATGCTCGTATGCGGAGACGACCTTGTGTTTATCTGTGAAGC	7609
Qy	6961	GCGGGACCCAGAGGACGAGCGAGCTACGGGCTTTCAGGAGGCTATGACTAGATAC	7020
Db	7610	GCGGGACCCAGAGGACGAGCGAGCTACGGGCTTTCAGGAGGCTATGACTAGATAC	7669
Qy	7021	TCTGCCCCCTTGGGACCCGCAAAACAGAAATAGACTTGGAGTTGATTAACATCATGC	7080
Db	7670	TCTGCCCCCTTGGGACCCGCAAAACAGAAATAGACTTGGAGTTGATTAACATCATGC	7729
Qy	7081	TCCTCCAATGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT	7140
Db	7730	TCCTCCAATGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT	7789
Qy	7141	GACCCACACCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAAT	7200
Db	7790	GACCCACACCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAAT	7849
Qy	7201	TCCTGGCTAGGCAACATCATGTATGCGGCCACTTGTGGGGAAGGATGATCTGATG	7260
Db	7850	TCCTGGCTAGGCAACATCATGTATGCGGCCACTTGTGGGGAAGGATGATCTGATG	7909
Qy	7261	ACTCATTTCTTCCATCTTCTAGCTCAGGAACAACTTGAAAGACCCCTAGATTGTGAG	7320
Db	7910	ACTCATTTCTTCCATCTTCTAGCTCAGGAACAACTTGAAAGACCCCTAGATTGTGAG	7969
Qy	7321	ATCTACGGGGCTGTACTTCCATTGAGCGACTTGACCTACCTCAGATCAATTCAGACTC	7380
Db	7970	ATCTACGGGGCTGTACTTCCATTGAGCGACTTGACCTACCTCAGATCAATTCAGACTC	8029
Qy	7381	CATGGCTTAGCGCATTTTCTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT	7440
Db	8030	CATGGCTTAGCGCATTTTCTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT	8089
Qy	7441	TCATGCTCAGGAACCTTGGGGTACCGGCTTGGCGAGTCTGGAGACATCGGGCCAGAGT	7500
Db	8090	TCATGCTCAGGAACCTTGGGGTACCGGCTTGGCGAGTCTGGAGACATCGGGCCAGAGT	8149
Qy	7501	GTCCGCGCTAGGCTACTGTCCCGGGGGGAGGGCTGCCACTTGTGGCAACTACTCTTC	7560
Db	8150	GTCCGCGCTAGGCTACTGTCCCGGGGGGAGGGCTGCCACTTGTGGCAACTACTCTTC	8209
Qy	7561	AACTGGGCGAGTAAGGACCAAGCTCAAACTCACTCCAATCCCGGCTGGCTCCAGTTGGAT	7620
Db	8210	AACTGGGCGAGTAAGGACCAAGCTCAAACTCACTCCAATCCCGGCTGGCTCCAGTTGGAT	8269
Qy	7621	TTATCCAGCTGGTTCGTGTGCTGTATCAGCGGGGGAGACATATATACAGGCTGTCTCGT	7680
Db	8270	TTATCCAGCTGGTTCGTGTGCTGTATCAGCGGGGGAGACATATATACAGGCTGTCTCGT	8329
Qy	7681	GCCCGACCCCGCTGCTGTGCTGTATCAGCGGGGGAGACATATATACAGGCTGTCTCGT	7740
Db	8330	GCCCGACCCCGCTGCTGTGCTGTATCAGCGGGGGAGACATATATACAGGCTGTCTCGT	8389
Qy	7741	CTACTCCCCAACCGATGAAACGGGAGGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTT	7800
Db	8390	CTACTCCCCAACCGATGAAACGGGAGGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTT	8449
Qy	7801	TTTCCC-----TTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	7850
Db	8450	TTTCCC-----TTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	8509
Qy	7851	TTCTCTCTTTTCT	7910
Db	8510	TTCTCTCTTTTCT	8569
Qy	7911	TAGTCACGGCTAGCTGTGAAAGGTCCTGAGCGCTTGTGAGTGTGAGTGTGAGTGTGAGT	7970
Db	8570	TAGTCACGGCTAGCTGTGAAAGGTCCTGAGCGCTTGTGAGTGTGAGTGTGAGTGTGAGT	8629
Qy	7971	GCCTCTCTGAGATCAAGT 7989	
Db	8630	GCCTCTCTGAGATCAAGT 8648	
RESULT 15			
US-10-029-907-4			
; Sequence 4, Application US/10029907			
; Patent No. 6706874			
; GENERAL INFORMATION:			
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.			
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM			
; FILE REFERENCE: 13/083			
; CURRENT APPLICATION NUMBER: US/10/029,907			
; CURRENT FILING DATE: 2001-12-21			
; PRIOR APPLICATION NUMBER: 60/257,857			
; PRIOR FILING DATE: 2000-12-22			
; NUMBER OF SEQ ID NOS: 25			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 4			
; LENGTH: 8643			
; TYPE: DNA			
; ORGANISM: HCV			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1802) ... (8407)			
US-10-029-907-4			
Query Match 90.4%; Score 7222.6; DB 4; Length 8643;			
Best Local Similarity 91.9%; Pred. No. 0;			
Matches 7953; Conservative 0; Mismatches 24; Indels 676; Gaps 4;			
Qy	2	CCAGCCCCCGATTGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGGAATCTACTGT	61
Db	2	CCAGCCCCCGATTGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGGAATCTACTGT	61
Qy	62	CTTCACGAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCTGTGAGGCTCCAGGACC	121
Db	62	CTTCACGAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCTGTGAGGCTCCAGGACC	121

QY	122	CCCTCTCCGGGAGAGCCATAGTGGTCTGCGGAACGGTGAATACACCGGAATTGCAGG	181	1190	AGACCAACACGGTTCCCTCTAGCGGATCAATTCGCCCCCTCTCCCTCCCCCCCCCCCTA	1249
Db	122	CCCCCTCCGGGAGAGCCATAGTGGTCTGCGGAACGGTGAATACACCGGAATTGCAGG	181	1202	AGACCAACACGGTTCCCTCTAGCGGATCAATTCG	1250
QY	182	ACGACCGGGTCTCTTTCTTGATCAACCCGCTCAATGCTGGAATTTGGCGTGCCTCCG	241	1250	ACGTTACTGGCCCGAAGCCGCTTGGAAATAGCGCGGTGTGCTGTATATATGTTATTTT	1309
Db	182	ACGACCGGGTCTCTTTCTTGATCAACCCGCTCAATGCTGGAATTTGGCGTGCCTCCG	241	1251	ACGTTACTGGCCCGAAGCCGCTTGGAAATAGCGCGGTGTGCTGTATATATGTTATTTT	1310
QY	242	CGAGACTGTAGCCGAGTAGTGTGGTCCGGAAGCCCTTGTGCTACTCCCTGATAGG	301	1310	CCACCATATTGCGCTCTTTTGGCAATGTAGGSCCGGAACCTGCGCTCTCTCTTGA	1369
Db	242	CGAGACTGTAGCCGAGTAGTGTGGTCCGGAAGCCCTTGTGCTACTCCCTGATAGG	301	1311	CCACCATATTGCGCTCTTTTGGCAATGTAGGSCCGGAACCTGCGCTCTCTCTTGA	1370
QY	302	TGCTTGGAGTGCCTCCGGGAGGTCTCGTAGCCGTGCACCATGAGCAGCATCTTAACC	361	1370	CGAGCATTCCTAGGGGTCTTTCCCTCTGCGCAAGGAATGCAAGTCTGTTGAATGTCG	1429
Db	302	TGCTTGGAGTGCCTCCGGGAGGTCTCGTAGCCGTGCACCATGAGCAGCATCTTAACC	361	1371	CGAGCATTCCTAGGGGTCTTTCCCTCTGCGCAAGGAATGCAAGTCTGTTGAATGTCG	1430
QY	362	TCAAGAAAAACCAAGGGCGCCATGATGAACAAAGATGGAATGGAATGGAATGGAATG	421	1430	TGAAGGAAGAGTTCCTCTGGAAGCTTTTGAAGAACAACAGCTGTAGAGACCCCTT	1489
Db	362	TCAAGAAAAACCAAGGGCGCCATGATGAACAAAGATGGAATGGAATGGAATGGAATG	421	1431	TGAAGGAAGAGTTCCTCTGGAAGCTTTTGAAGAACAACAGCTGTAGAGACCCCTT	1490
QY	422	GGCGCTTGGTGGAGAGGTATTCGGCTATGACTGGGCAACAGACATCGCTGCTC	481	1490	GAGGAGCGGAAACCCACCTGGCGACAGTGCCTCTGCGGCCAAAGACCGCTGAT	1549
Db	422	GGCGCTTGGTGGAGAGGTATTCGGCTATGACTGGGCAACAGACATCGCTGCTC	481	1491	GAGGAGCGGAAACCCACCTGGCGACAGTGCCTCTGCGGCCAAAGACCGCTGAT	1550
QY	482	TGATGCCGCGTGTCCGGCTGTACGCGCAGGGCGCCCGTCTTTTGTCAAGACCGA	541	1550	AAGATACACTGCAAAAGGGCGCACAAACCCAGTGCACCTGTGAGTTGATGTTGCTG	1609
Db	482	TGATGCCGCGTGTCCGGCTGTACGCGCAGGGCGCCCGTCTTTTGTCAAGACCGA	541	1551	AAGATACACTGCAAAAGGGCGCACAAACCCAGTGCACCTGTGAGTTGATGTTGCTG	1610
QY	542	CTGTCCGTGCTGCTGAATGAATGCAAGGAGGAGGCGCGCTATGCTGCAAGAC	601	1610	AAGAGTCAATGCGTCTCTCAAGCGTATTCAAAGGGGCTGAAGATGCCCAGAGG	1669
Db	542	CTGTCCGTGCTGCTGAATGAATGCAAGGAGGAGGCGCGCTATGCTGCAAGAC	601	1611	AAGAGTCAATGCGTCTCTCAAGCGTATTCAAAGGGGCTGAAGATGCCCAGAGG	1670
QY	602	GAGCGGCTTCTTGGCGAGTGTGCTGCAAGGCTGCTGCTGCTGCTGCTGCTGCTG	661	1670	TACCCCATTTGATGGGATCTGATCTGGGCGCTCGGTGCACTGTTTACATGTTTGTAGT	1729
Db	602	GAGCGGCTTCTTGGCGAGTGTGCTGCAAGGCTGCTGCTGCTGCTGCTGCTGCTG	661	1671	TACCCCATTTGATGGGATCTGATCTGGGCGCTCGGTGCACTGTTTACATGTTTGTAGT	1730
QY	662	GCTATTGGGCGAAGTCCCGGGCAGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTG	721	1730	CGAGGTTAAACACGCTTAGGGCCCCCGAACCAACCGGGGACGTGTTTCTTTGAAAAAC	1789
Db	662	GCTATTGGGCGAAGTCCCGGGCAGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTG	721	1731	CGAGGTTAAACACGCTTAGGGCCCCCGAACCAACCGGGGACGTGTTTCTTTGAAAAAC	1790
QY	722	AGTATCCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	781	1790	ACGATTAATACCATG	1803
Db	722	AGTATCCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	781	1791	ACGATAATACCATGGACCGGGAGATGGCAGCATCGTGGGAGGCGCGGTTTTCGTAGGTC	1850
QY	782	ATTGACCAACCAAGCAACATCGCATCGAGCGAGCAGTACGATGGAAGCGGCTCT	841	1804	-----	1803
Db	782	ATTGACCAACCAAGCAACATCGCATCGAGCGAGCAGTACGATGGAAGCGGCTCT	841	1851	TGATACTCTTGACCTTGTCACCGCACTATAAGCTGTTCTCGTAGGCTCATATGTTGTT	1910
QY	842	TGTCGATCAGGATGATCTGGAAGAGCAGATCAGGGGCTCGCGCCAGCGAACTGTCG	901	1804	-----	1803
Db	842	TGTCGATCAGGATGATCTGGAAGAGCAGATCAGGGGCTCGCGCCAGCGAACTGTCG	901	1911	TACATATTTTATACAGGGCGGAGGCACACTTGCAGTGTGATGCCCCCTCAACG	1970
QY	902	CAGGCTCAAGGCGCGATGCGCGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG	961	1804	-----	1803
Db	902	CAGGCTCAAGGCGCGATGCGCGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG	961	1971	TTTGGGGGGGCGCGATGCGCTCATCTCTCTCACTGCGCGATCCACCCAGAGCTAATCT	2030
QY	962	CTTGCGCAATATCATGGTGGAAATGCGCGCTTTTCTGGAATTCATGCTGCGCGGCT	1021	1804	-----	1803
Db	962	CTTGCGCAATATCATGGTGGAAATGCGCGCTTTTCTGGAATTCATGCTGCGCGGCT	1021	2031	TTACCATCACCAAAATCTTGTGCGCATACTCGGTCCACTCATGTTGCTCCAGGCTGGTA	2090
QY	1022	GGGTGTGGCGGACCGCTATCAGSACATAGCGTGTGGCTACCCGCTGATATTGCTGAAG	1081	1804	-----	1803
Db	1022	GGGTGTGGCGGACCGCTATCAGSACATAGCGTGTGGCTACCCGCTGATATTGCTGAAG	1081	2091	TAAACAAAGTGGTACTTTCTGTCGCGGCACACGGGCTCATTCGTGTCATGTCGCTGTC	2150
QY	1082	TGGCGCGAATGGCTGACCGCTTCTGCTGCTTACGATGCGCGCTCCCGATTGCA	1141	1804	-----	1803
Db	1082	TGGCGCGAATGGCTGACCGCTTCTGCTGCTTACGATGCGCGCTCCCGATTGCA	1141	2151	GGAAGTTGCTGGGGTCAATATGTCCAAATGGCTCTCATGAAGTTGGCGGCATGACAG	2210
QY	1142	GCGCATCGCTTCTATCGCTTCTTGAACAGTCTTCTGAGTT-----TAAAC	1189	1804	-----	1803
Db	1142	GCGCATCGCTTCTATCGCTTCTTGAACAGTCTTCTGAGTTCTTCTGAGTTGCGCGCCAGATGTAAC	1201	2211	GTACGTACGTTTATGACCATCTCACCCACTGCGGAGCTGGGCCACCGGGCTACGAG	2270

Db 2271 ACCTTGGGTGGCAGTGTGAGCCCGTCTGCTTCTCTGATATGAGAGCAAGGTTATCACT 2330  
 QY 1804 ----- 1803  
 Db 2331 GGGGGGACAGACACCGCGGTGTGGGGACATCATCTTGGGCCGTGCCGCTCTCCGCCGCA 2390  
 QY 1804 ----- 1803  
 Db 2391 GGGGAGGAGATACATCTGGGACCGGACAGAGCCTTGAAGGGCAGGGTGGGACTCC 2450  
 QY 1804 --GCOCCTATTACGCCCTACTCCCAACAGACGCGAGGCCCTACTTGGCTGCATCACTA 1861  
 Db 2451 TCGCGCCTATTACGCCCTACTCCCAACAGACGCGAGGCCCTACTTGGCTGCATCACTA 2510  
 QY 1862 GCCTCACAGGCGGACAGGACAGGACCGAGGTGAGGGGGAGGTCAAGTGTCTCCACCGCA 1921  
 Db 2511 GCCTCACAGGCGGACAGGAAACGAGGTGAGGGGGAGGTCCAAAGTGTCTCCACCGCA 2570  
 QY 1922 CACAATCTTCTGGGACCTCGTCAATGGCGTGTGTTGGACTGTCTATCATGTGCGG 1981  
 Db 2571 CACAATCTTCTGGGACCTCGTCAATGGCGTGTGTTGGACTGTCTATCATGTGCGG 2630  
 QY 1982 GCTCAAGACCTTCCCGGCCCAAGGGGCCAATCACCCAAATGTACACCAATGTGGACC 2041  
 Db 2631 GCTCAAGACCTTCCCGGCCCAAGGGGCCAATCACCCAAATGTACACCAATGTGGACC 2690  
 QY 2042 AGGACCTCGTGGCTGGCAAGCGCCCGCGGGCGGTTCTTGACCATGCACTGGG 2101  
 Db 2691 AGGACCTCGTGGCTGGCAAGCGCCCGCGGGCGGTTCTTGACCATGCACTGGG 2750  
 QY 2102 GCAGCTCGGACCTTACTTGGTTCAGAGCATGCGCATCTCCGGTGGCCCGCGGG 2161  
 Db 2751 GCAGCTCGGACCTTACTTGGTTCAGAGCATGCGCATCTCCGGTGGCCCGCGGG 2810  
 QY 2162 GCGACAGAGGGGGAGCTACTCTCCCCAGGCCCGTCTCTACTTGAAGGCTCTTCGG 2221  
 Db 2811 GCGACAGAGGGGGAGCTACTCTCCCCAGGCCCGTCTCTACTTGAAGGCTCTTCGG 2870  
 QY 2222 GCGGTCCATGCTCTGCCCTCGGGGACGCTGTGGGCATCTTTCGGGTGGCGGTGCA 2281  
 Db 2871 GCGGTCCATGCTCTGCCCTCGGGGACGCTGTGGGCATCTTTCGGGTGGCGGTGCA 2930  
 QY 2282 CCCGAGGGGTTCCGAGGGGGTGGACTTTGTATCCCGTCCAGTCTATGGAACCACTATGC 2341  
 Db 2931 CCCGAGGGGTTCCGAGGGGGTGGACTTTGTATCCCGTCCAGTCTATGGAACCACTATGC 2990  
 QY 2342 GGTCCCGGTCTTCCAGACAACTCGTCCCTCCGCGCGTACCGAGACATTCAGGTGG 2401  
 Db 2991 GGTCCCGGTCTTCCAGACAACTCGTCCCTCCGCGCGTACCGAGACATTCAGGTGG 3050  
 QY 2402 CCATCTACAGCCCTACTGTAGGGGCAAGACCTAAGGTGGCGGCTGGTATGCA 2461  
 Db 3051 CCCATCTACAGCCCTACTGTAGGGGCAAGACCTAAGGTGGCGGCTGGTATGCA 3110  
 QY 2462 CCCAAGGGTATAAGGTGCTTGTCTTGAACCCGCTCGGTCCCGCCACCCCTAGGTTCGGGG 2521  
 Db 3111 CCCAAGGGTATAAGGTGCTTGTCTTGAACCCGCTCGGTCCCGCCACCCCTAGGTTCGGGG 3170  
 QY 2522 CGTATATGTTAAGGCATATGTTATCGACCCCTAAACATCAGAACCGGGGTAAAGCAATCA 2581  
 Db 3171 CGTATATGTTAAGGCATATGTTATCGACCCCTAAACATCAGAACCGGGGTAAAGCAATCA 3230  
 QY 2582 CCACGGGTGCCCCCATCAGTACTCCACCTATGGCAAGTTTCTTCCGAGCGGTGGTGTCT 2641  
 Db 3231 CCACGGGTGCCCCCATCAGTACTCCACCTATGGCAAGTTTCTTCCGAGCGGTGGTGTCT 3290  
 QY 2642 CTGGGGGCGCTTATGACATCAATAATGTGATGAGTGCCACTCAACTGACTCGACCACTA 2701  
 Db 3291 CTGGGGGCGCTTATGACATCAATAATGTGATGAGTGCCACTCAACTGACTCGACCACTA 3350  
 QY 2702 TCTTGGGCATCGGCACAGTCTCTGGACCAAGCGGAGACGCTGGAGCGGACTCGTGTGC 2761

Db 3351 TCCTGGGCATCGGCACAGTCTCTGGACCAAGCGGAGACGCTGGAGCGGACTCTGCTGTC 3410  
 QY 2762 TCGCCACCGCTACCGCTCCGGGATCGGTACCGTCCACATCCCAACATCCGAGGAGGTGG 2821  
 Db 3411 TCGCCACCGCTACCGCTCCGGGATCGGTACCGTCCACATCCCAACATCCGAGGAGGTGG 3470  
 QY 2822 CTCTCTCAGCACTGGAGAAATCCCTTTTATGTCGAAAGCCATCCCATCCGAGACCATCA 2881  
 Db 3471 CTCTCTCAGCACTGGAGAAATCCCTTTTATGTCGAAAGCCATCCCATCCGAGACCATCA 3530  
 QY 2882 AGGGGGGAGGACCTCATTTTCTGCCATTCGAAAGAAATGTGATGAGCTCGCGCGA 2941  
 Db 3531 AGGGGGGAGGACCTCATTTTCTGCCATTCGAAAGAAATGTGATGAGCTCGCGCGA 3590  
 QY 2942 AGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTCGCGGGCTTGAATGATCCGTCA 3001  
 Db 3591 AGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTCGCGGGCTTGAATGATCCGTCA 3650  
 QY 3002 TACCAACTAGCGGAGACGCTCATTTGTGTAGCAACGAGCGCTCTAATGACGGGCTTTACCG 3061  
 Db 3651 TACCAACTAGCGGAGACGCTCATTTGTGTAGCAACGAGCGCTCTAATGACGGGCTTTACCG 3710  
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 Db 3771 TGGACCCGACCTTACCATTTGAGAGACGACGCGTCCCAAGACGCGGTGTCAACGCTCGC 3830  
 QY 3182 AGCGCGAGGAGGACGCTGTAGGGGACGATGGGCAITTTACAGGTTTGTGACTCCAGGAG 3241  
 Db 3831 AGCGCGAGGAGGACGCTGTAGGGGACGATGGGCAITTTACAGGTTTGTGACTCCAGGAG 3890  
 QY 3242 AACGGCCCTCGGGCATGTTGATTTCTCGTTCTGTGCGAGTGTATGACGCGGGCTGTG 3301  
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 QY 3302 CTTGTGTAGAGCTACGCGCCGCGAGACCTCAGTTAGTTGCGGGCTTACCTTAAACACAC 3361  
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 QY 3722 TCCTAGAGCTCTGCGCGGCTATTCCTGACAAACAGGAGCGGTGTGCTTGTGGGAGGAG 3781  
 Db 4371 TCCTAGAGCTCTGCGCGGCTATTCCTGACAAACAGGAGCGGTGTGCTTGTGGGAGGAG 4430  
 QY 3782 TCATCTGTCCGAAAGCGCGGCTATTCCTCCGACAGGGAAGTCTCTTTACCGGGAGTTGG 3841  
 Db 4431 TCATCTGTCCGAAAGCGCGGCTATTCCTCCGACAGGGAAGTCTCTTTACCGGGAGTTGG 4490

Qy	3842	ATGAGATGGAAGAGTGGCGCTCACACCTCCCTTACATCGAACAGGGAATGAGCTCGCG	3901	Qy	4922	CCACGGCCCTCTGACAGCCCTCCCGCGCCCAAAATTATTTAGGGCGCTGTGGCGGTGG	4981
Db	4491	ATGAGATGGAAGAGTGGCGCTCACACCTCCCTTACATCGAACAGGGAATGAGCTCGCG	4550	Db	5571	CCACGGCCCTCTGACAGCCCTCCCGCGCCCAAAATTATTTAGGGCGCTGTGGCGGTGG	5630
Qy	3902	AACAATTCAAACAGAGGCAATCGGTTGCTGCAAAACAGCCACCAAGCAGCGAGCTG	3961	Qy	4982	CTGCTGAGGAGTACGTGGAGGTTACGGGTTGCGGGATTTTCCACTACGTGACCGGCAATGA	5041
Db	4551	AACAATTCAAACAGAGGCAATCGGTTGCTGCAAAACAGCCACCAAGCAGCGAGCTG	4610	Db	5631	CTGCTGAGGAGTACGTGGAGGTTACGGGTTGCGGGATTTTCCACTACGTGACCGGCAATGA	5690
Qy	3962	CTGCTCCCGTGGTGGATCCAAAGTGGCGGACCTCGAAGCCCTTCTGGCGGAGCATATGT	4021	Qy	5042	CCACTGACAAAGTAAAGTGGCCGCTCAGGTTCCGGGCCCCCGAATTTCTTACACAAGTGG	5101
Db	4611	CTGCTCCCGTGGTGGATCCAAAGTGGCGGACCTCGAAGCCCTTCTGGCGGAGCATATGT	4670	Db	5691	CCACTGACAAAGTAAAGTGGCCGCTCAGGTTCCGGGCCCCCGAATTTCTTACACAAGTGG	5750
Qy	4022	GGATTTTCATCAGCGGGATACAATATTTAGCAGGCTTGTCACATCTGCTGGCAACCCCG	4081	Qy	5102	ATGGGGTGGCGTTGCACAGGTACGCTCCAGCGTCAAAACCCCTCTTACGGGAGGAGTCA	5161
Db	4671	GGATTTTCATCAGCGGGATACAATATTTAGCAGGCTTGTCACATCTGCTGGCAACCCCG	4730	Db	5751	ATGGGGTGGCGTTGCACAGGTACGCTCCAGCGTCAAAACCCCTCTTACGGGAGGAGTCA	5810
Qy	4082	CGATAGCATCACTGATGGCAATTCAGCTCTATACAGCGCCGCTCAACCAACAAATA	4141	Qy	5162	CATTCTCTGCTGGGCTCAATCAATACTCTGGTTGGGTCAACAGTCCCATTCGAGCCGGAAC	5221
Db	4731	CGATAGCATCACTGATGGCAATTCAGCTCTATACAGCGCCGCTCAACCAACAAATA	4790	Db	5811	CATTCTCTGCTGGGCTCAATCAATACTCTGGTTGGGTCAACAGTCCCATTCGAGCCGGAAC	5870
Qy	4142	CCCTCCCTGTTTAAATCCTCGGGGGATGGGTGGCGCCCAACTTGTCTCCCAAGCGCTG	4201	Qy	5222	CGGACGTAGCAGTGTCTCACTTCCATGCTCACCGACCCCTCCCATTTACGGCGGAGCGG	5281
Db	4791	CCCTCCCTGTTTAAATCCTCGGGGGATGGGTGGCGCCCAACTTGTCTCCCAAGCGCTG	4850	Db	5871	TGGACGTAGCAGTGTCTCACTTCCATGCTCACCGACCCCTCCCATTTACGGCGGAGCGG	5930
Qy	4202	CTTCTGCTTTCTGTAAGCGCGCGCATCGCTGGAGCGGCTGTTGGCAGCATAGGCCCTTGGGA	4261	Qy	5282	CTAAGCGTAGGCTGGCCAGGGGATCTCCCCCTCTCTTGGCGAGCTCATAGCTAGCCAGC	5341
Db	4851	CTTCTGCTTTCTGTAAGCGCGCGCATCGCTGGAGCGGCTGTTGGCAGCATAGGCCCTTGGGA	4910	Db	5931	CTAAGCGTAGGCTGGCCAGGGGATCTCCCCCTCTCTTGGCGAGCTCATAGCTAGCCAGC	5990
Qy	4262	AGTGTCTTGGATATTTTGGCAGGTTATGGAGCAGGGGTGGAGCGCGCTCTGTGGCCT	4321	Qy	5342	TGCTTGGCGCTTCTTGAAGGAAATGACATACCGTCACTACCGTCACTCCCGGACCGTGAAC	5401
Db	4911	AGTGTCTTGGATATTTTGGCAGGTTATGGAGCAGGGGTGGAGCGCGCTCTGTGGCCT	4970	Db	5991	TGCTTGGCGCTTCTTGAAGGAAATGACATACCGTCACTACCGTCACTCCCGGACCGTGAAC	6050
Qy	4322	TTAAGGTCATGAGCGGCGAGATGCCCTCCACCGAGGACCTGGTTAACTACTCCCTGCTA	4381	Qy	5402	TCATTCGAGGCAACCTCTCTGTGGCGGAGAGATGGCGGGGAAATCAACCCGCTGGAGT	5461
Db	4971	TTAAGGTCATGAGCGGCGAGATGCCCTCCACCGAGGACCTGGTTAACTACTCCCTGCTA	5030	Db	6051	TCATTCGAGGCAACCTCTCTGTGGCGGAGAGATGGCGGGGAAATCAACCCGCTGGAGT	6110
Qy	4382	TCCTCTCCCTGGCGCCTAGTCTCGGGGTCTGTGCGCAGCGATATCTGCTGGCGACG	4441	Qy	5462	CAGAAAATAAGGTAGTAAATTTTGGACTCTTTTGGAGCGCTCCAAAGCGGAGGAGATGAGA	5521
Db	5031	TCCTCTCCCTGGCGCCTAGTCTCGGGGTCTGTGCGCAGCGATATCTGCTGGCGACG	5090	Db	6111	CAGAAAATAAGGTAGTAAATTTTGGACTCTTTTGGAGCGCTCCAAAGCGGAGGAGATGAGA	6170
Qy	4442	TGGGCCCGAGGAGGGGCTGTGAGTGGATGAACCGGCTGATAGCGTTGCTTGGCGGG	4501	Qy	5522	GGGAGTATCGTTTCCGGCGGAGATCTGCGGAGGTCCAGGAAATTTCTCTGAGCGATGC	5581
Db	5091	TGGGCCCGAGGAGGGGCTGTGAGTGGATGAACCGGCTGATAGCGTTGCTTGGCGGG	5150	Db	6171	GGGAGTATCGTTTCCGGCGGAGATCTGCGGAGGTCCAGGAAATTTCTCTGAGCGATGC	6230
Qy	4502	GTAACACGCTCTCCCGCACCATATCTGCTGAGAGCAGCGCTGACAGCAGCTGCTCACTC	4561	Qy	5582	CCATATGGGCACCGCGGATTTACAAACCTCCACTGTTTAGAGTCTCTGAAAGAACCCGACT	5641
Db	5151	GTAACACGCTCTCCCGCACCATATCTGCTGAGAGCAGCGCTGACAGCAGCTGCTCACTC	5210	Db	6231	CCATATGGGCACCGCGGATTTACAAACCTCCACTGTTTAGAGTCTCTGAAAGAACCCGACT	6290
Qy	4562	AGATCTCTCTAGTCTTACCATCACTCAGCTGCTGTAAGAGGCTTTACAGTGGATCAACG	4621	Qy	5642	ACGTCCCTCCAGTGGTACACGGGTGTCATTGGCGCTCCAAAGGCCCTCCGATACCAAC	5701
Db	5211	AGATCTCTCTAGTCTTACCATCACTCAGCTGCTGTAAGAGGCTTTACAGTGGATCAACG	5270	Db	6291	ACGTCCCTCCAGTGGTACACGGGTGTCATTGGCGCTCCAAAGGCCCTCCGATACCAAC	6350
Qy	4622	AGGACTGCTCCAGCCATGCTCGGCTCTGCTGCTGAGAGATGTTTGGGATGGATATGCA	4681	Qy	5702	CTCCACGGAGAGAGGACGGTTGCTCTGTTCAGATCTACCGTGTCTTCTGCTTGGCGG	5761
Db	5271	AGGACTGCTCCAGCCATGCTCGGCTCTGCTGCTGAGAGATGTTTGGGATGGATATGCA	5330	Db	6351	CTCCACGGAGAGAGGACGGTTGCTCTGTTCAGATCTACCGTGTCTTCTGCTTGGCGG	6410
Qy	4682	CGGTGTTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGCTCTCCGCGGATTTGCGGGAG	4741	Qy	5762	AGCTCGGCACAAAGACCTTCGGCAGCTCCCAATCTCGTGGCGCTCGACAGCGGCAACGCAA	5821
Db	5331	CGGTGTTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGCTCTCCGCGGATTTGCGGGAG	5390	Db	6411	AGCTCGGCACAAAGACCTTCGGCAGCTCCCAATCTCGTGGCGCTCGACAGCGGCAACGCAA	6470
Qy	4742	TCCCTCTTCTCATGTCAACAGTGGGTACAAGGAGTCTTGGCGGGCGAGCGCATATGC	4801	Qy	5822	CGGCTCTCTGACAGCCCTCCGACGACGGCGACCGGGATCCGATCTCAGCGGCTGCTACT	5881
Db	5391	TCCCTCTTCTCATGTCAACAGTGGGTACAAGGAGTCTTGGCGGGCGAGCGCATATGC	5450	Db	6471	CGGCTCTCTGACAGCCCTCCGACGACGGCGACCGGGATCCGATCTCAGCGGCTGCTACT	6530
Qy	4802	AAACCACTGCCATGTGGAGCAGATCACCGACATGTGAAACCGTTTCCATGAGGA	4861	Qy	5882	CCTCCATGCCCCCTTGGAGGGGAGCCGGGGATCCCGATCTCAGCGGCTGCTGGT	5941
Db	5451	AAACCACTGCCATGTGGAGCAGATCACCGACATGTGAAACCGTTTCCATGAGGA	5510	Db	6531	CCTCCATGCCCCCTTGGAGGGGAGCCGGGGATCCCGATCTCAGCGGCTGCTGGT	6590
Qy	4862	TCGTGGGCGCTTAGGACCTGTAGTAAACACGCTGGCATGGAACATTTCCCATTAACGCTACA	4921	Qy	5942	CTACCGTAAAGCAGGAGGCTTAGTGGAGACGTCGCTGCTGCTCGATGCTCTACACATGGA	6001
Db	5511	TCGTGGGCGCTTAGGACCTGTAGTAAACACGCTGGCATGGAACATTTCCCATTAACGCTACA	5570	Db	6591	CTACCGTAAAGCAGGAGGCTTAGTGGAGACGTCGCTGCTGCTCGATGCTCTACACATGGA	6650
				Qy	6002	CAGCGGCCCTGATCAAGCCATGCGCTGCGGAGGAAACCAAGCTGCCCATCAATGACATGA	6061

Db 6651 CGGGCCCTGATCAGCCATGCGCTGCGGAGGAAACCAAGCTGCCATCAATGCACTGA 6710  
Qy 6662 GCACTCTTTGTCGCTGACCAACAATTGCTTATGCTTACAACTCTCGAGCGCAAGCC 6121  
Db 6711 GCACTCTTTGTCGCTGACCAACAATTGCTTATGCTTACAACTCTCGAGCGCAAGCC 6770  
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Qy 6182 TGCTCAAGAGATGAAGCGGAGGCGTCCACAGTTAAGGCTAAACTTCTATCCGTGGAGG 6241  
Db 6831 TGCTCAAGAGATGAAGCGGAGGCGTCCACAGTTAAGGCTAAACTTCTATCCGTGGAGG 6890  
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Db 6951 AAGTCCGGAACCTATCCAGCAAGGCGTTTAAACACATCCGCTCCGCTGGAAGGACTTGC 7010  
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Qy 6422 TCCAAACAGAGAGAGGCGGCCAGCAGCTCGCTTATCGTATCCAGATTTGGGGG 6481  
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Qy 6782 CTAAATCTAAAGGAGAACTGGGCTATGCGGCTATGCGCGGCGGAGGCTGACTGACGA 6841  
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Db 7551 AGCTCCAGGACTGCAGATGCTGCTATGCGGAGACGACCTTGTGTTATCTGTGAAAGCG 7610  
Qy 6962 CGGGGACCCAAAGAGAGAGGCGGCTAGCGGCTTACGGAGGCTATGACTAGTACT 7021  
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Db 8151 TCCGCGCTAGGCTACTGCTCCAGGGGGAGGCTGCCACTTGTGGCAAGTACCTCTTCA 8210  
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Db 8451 TCCCTT 8510  
Qy 7859 --TTTTTTTTCTT 7916  
Db 8511 TCTTTTTTCCCAATT 8570  
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Db 8571 CCGCTAGCTGTGAAGGTCCTGAGCGCTTGACTGACAGAGAGTGTGATCTGGGCTCT 8630  
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Job time : 683 secs



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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_hcg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pi.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7992	100.0	10690	6	AX739972 Sequence
2	7989	100.0	7989	6	AR406043 Sequence
3	7989	100.0	7989	6	AX036255 Sequence
4	7989	100.0	7989	12	SSB242652
5	7967	99.7	8001	6	AR406042 Sequence
6	7967	99.7	8001	6	AX036254 Sequence
7	7967	99.7	8001	12	SSB242654
8	7949.4	99.5	8001	6	AR406047
9	7949.4	99.5	8001	6	AX036259
10	7947.8	99.4	8001	6	AR406045
11	7947.8	99.4	8001	6	AX036257
12	7941.4	99.4	8001	6	AR406049
13	7941.4	99.4	8001	6	AX036261
14	7611.8	95.2	12305	6	AX937622
15	7608.6	95.2	12315	6	AX937621
16	7331	91.7	8637	6	AR406041
17	7331	91.7	8637	6	AX036253
18	7331	91.7	8637	12	SSB242651
19	7309	91.5	8649	6	AR406044

20	7309	91.5	8649	6	AX036256	Sequence
21	7309	91.5	8649	12	SSB242653	Hepatitis
22	7273.8	91.0	8639	6	AR488100	Sequence
23	7273.8	91.0	8639	6	AX472291	Sequence
24	7272.8	91.0	8638	6	AR488121	Sequence
25	7272.8	91.0	8638	6	AX472314	Sequence
26	7249.8	90.7	8638	6	AR488105	Sequence
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28	7248.8	90.7	8638	6	AR488122	Sequence
29	7248.8	90.7	8638	6	AX472315	Sequence
30	7246.8	90.7	8642	6	AR488101	Sequence
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33	7245.6	90.7	8638	6	AX472296	Sequence
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35	7229.8	90.5	8648	6	AX472295	Sequence
36	7222.6	90.4	8643	6	AR488102	Sequence
37	7222.6	90.4	8643	6	AX472294	Sequence
38	6681.4	83.6	9658	14	AB113282	Sequence
39	6186.8	77.4	9605	6	AX739971	Hepatitis
40	6186.8	77.4	9605	14	HCJ238799	Sequence
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43	6169.2	77.2	11076	6	AR406048	Sequence
44	6169.2	77.2	11076	6	AX036260	Sequence
45	6167.6	77.2	11076	6	AR406046	Sequence

## ALIGNMENTS

RESULT 1  
AX739972  
LOCUS AX739972 10690 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 3 from Patent WO02059321.  
ACCESSION AX739972  
VERSION AX739972.1 GI:30519246  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS de Francesco, R., Migliaccio, G. and Paonessa, G.  
TITLE Hepatitis C virus replicons and replicon enhanced cells  
JOURNAL Patent: WO 02059321-A 3 01-AUG-2002;  
ISTITUTO DI RICERCHE DI BIOLOGIA MOLECOLARE P. ANGELETTI S.P.A.  
(IT)

FEATURES  
source Location/Qualifiers  
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/note="pHCVNeo.17 coding"

## ORIGIN

Query Match 100.0%; Score 7992; DB 6; Length 10690;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 7992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 GCCAGCCCCCGATTGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAACACTG 60  
QY 61 TCTTACGAGAGAGCGTCTAGCCATGGGCTTAGTATGAGTGTGTCGTCGACCTCCAGGAC 120  
Db 61 TCTTACGAGAGAGCGTCTAGCCATGGGCTTAGTATGAGTGTGTCGTCGACCTCCAGGAC 120  
QY 121 CCCCCCTCCGGAGAGCGCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTCGCG 180  
Db 121 CCCCCCTCCGGAGAGCGCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTCGCG 180  
QY 181 GACGACCGGTCCTTCTTCTTGGATACACCGCTCATGCTGAGATTGGCGTGCCTCC 240

Db 181 GACGACCGGTCCTTTCTTTGATCAACCCGCTCAATGCTGAGATTTGGGCTGCCCCC 240  
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Db 241 GCGAGACTGCTAGCCGAGTAGTGTGGTTCGGAAGCCCTTGTGGTACTGCTGATAGG 300  
Qy 301 GTGCTTGGAGTGCCCGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCTTAAC 360  
Db 301 GTGCTTGGAGTGCCCGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCTTAAC 360  
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Db 841 TTGTGATCAGGATGATCTGGAAGAGAGCATCAGGGGCTCGGCGAGCGAACTGTTGC 900  
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QY 4501 GGTAAACAGTCTCCCGCAGCATATGCTCTGAGAGCGACGCTGAGCAGCATGCTCACT 4560  
DB GGTAAACAGTCTCCCGCAGCATATGCTCTGAGAGCGACGCTGAGCAGCATGCTCACT 4560  
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Qy	4681	GAGGACTGCTCAGCCGATGCTCCGGCTCGTGGCTTAAGAGATGTTTGGGATTGGATATGC	4740
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Qy	5581	CCCATATGGGACGCCCGGATTAACAACTTCACTGTTAGTCTCTGGAAGGACCCCGGAC	5640
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Qy	5641	TACGTCCCTCCAGTGTACAGGCTGTCATTGCGCTGCCAAGGCCCTCCCATACCA	5700
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Qy	5701	CCTCAACGGAAGAGACGGTTTCTCTGTGAGAAATCTACCGTGTCTTCTGCTTGGCG	5760
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Qy	5761	GAGTCTGCCCAAAAGACCTTCCGAGCTCCGAATCGTGGCGCTCGACAGCGGACCGCA	5820
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Qy	5821	ACGGGCTCTCTGACAGCCCTCCGACGACGCGGAGTCCGATCTCAGCGACGGTCTTGG	5880
Db	5821		5880
Qy	5881	TCCTCATGCCCCCTTGAAGGGGAGCGCGGGGATCCCGATCTCAGCGACGGGCTTGG	5940
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Qy	5941	TCCTCATGCCCCCTTGAAGGGGAGCGCGGGGATCCCGATCTCAGCGACGGTCTTGG	6000
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Qy	6001	ACAGGCGCCCTGATCACGCCATGCGCTGCGAGGAAACCAAGCTGCCATCAATCAACTG	6060
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Qy	6181	GTGCTCAAGAGATGAAGCGGAAGCGTCCACAGTTAAGGTAAATCTCTATCCGTGGAG	6240
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Qy	6241	GAAGCCTGTAAAGTGAAGCGGAAAGCGTCCACAGTTAAGGTAAATCTCTATCCGTGGAG	6300
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Qy	6301	GAGTCCGGAACCTATTCAGAGAGCGCTTAAACCATCGCTCCGTGTGGAAGGACTTG	6360
Db	6301		6360
Qy	6361	CTGGAAGACACTGAGACACCAATTGACACCAATCATGGCAAAATAGGTTTCTGTC	6420
Db	6361		6420
Qy	6421	GTCCAAACGAGAGGGGGCGCAAGCCAGCTCGGCTTATCGTATTTCCAGATTGGGG	6480
Db	6421		6480
Qy	6481	GTTCGTGTGTCGAGAAATGGCCCTTACAGTGTGTCTCCACCTCTCCCTCAGGCGCTG	6540
Db	6481		6540
Qy	6541	ATGGGCTCTTTCATACGGAATTTCCAATACTCTCTGGGAGCGGCTCGAGTCTCTGGTGAAT	6600
Db	6541		6600
Qy	6601	GCCTGGAAGCGAAGAAATGCCCTATGGGCTTCGCATATGACACCGCTGTTTGAATCA	6660
Db	6601		6660
Qy	6661	ACGCTCACTGAGATGACATCCGTTGTGAGGAGTCAATCTACCAATTTGTGACTTGGCC	6720
Db	6661		6720
Qy	6721	CCGGAAGCCAGACAGGCCATTAAGTCCGCTCAGAGCGGCTTTTACATCGGGGGCCCCCTG	6780
Db	6721		6780



Db	541		ACCTGTCGGTCCCTGATGAATCTGCAGGACGAGCGGGCTATGTCGCTGGCCA	600	Db	1621	TGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCAGAGGTACCCCATTCG	1680
Qy	601		CGACGGGGTTCCTTGCAGCTGTGCTCGAAGCTGTGTCTCAAGCGGGAAGGACTGCG	660	Qy	1681	ATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTTACATGTGTTTGTAGTCGAGGTAAAA	1740
Db	601		CGACGGGGTTCCTTGCAGCTGTGCTCGAAGCTGTGTCTCAAGCGGGAAGGACTGCG	660	Db	1681	ATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTTACATGTGTTTGTAGTCGAGGTAAAA	1740
Qy	661		TGCTATTGGGCGAAGTGC CGGGGAGGATCTCTGTCACTCACCTTGTCTCTGCCGAGA	720	Qy	1741	AAAGCTCTAGGCCCCCGAACAACGAGGAGCTGGTTCCTTTGAAAAACACGATATACC	1800
Db	661		TGCTATTGGGCGAAGTGC CGGGGAGGATCTCTGTCACTCACCTTGTCTCTGCCGAGA	720	Db	1741	AAAGCTCTAGGCCCCCGAACAACGAGGAGCTGGTTCCTTTGAAAAACACGATATACC	1800
Qy	721		AAGTATCCATCATGGCTGATCAATGCGGGGCTGCATACGCTTGATCCGGTACCTGCC	780	Qy	1801	ATGGGCGCTATTACGGCTTACTCCCAACAGAGCGAGGGCTACTTGGCTGCAATCATCT	1860
Db	721		AAGTATCCATCATGGCTGATCAATGCGGGGCTGCATACGCTTGATCCGGTACCTGCC	780	Db	1801	ATGGGCGCTATTACGGCTTACTCCCAACAGAGCGAGGGCTACTTGGCTGCAATCATCT	1860
Qy	781		CATTGACACCAAGCGAACAATCGCATCGAGGAGCAGTACTCGGATGGAAGCCGGTC	840	Qy	1861	ASCTTACAGGCGGGGACAGGAACAGAGTCTGAGGGGAGGTCCAAAGTGTCTCCACCGCA	1920
Db	781		CATTGACACCAAGCGAACAATCGCATCGAGGAGCAGTACTCGGATGGAAGCCGGTC	840	Db	1861	ASCTTACAGGCGGGGACAGGAACAGAGTCTGAGGGGAGGTCCAAAGTGTCTCCACCGCA	1920
Qy	841		TTGTCGATCAGGATGATCTGGAAGAGATCAGGGGCTCGGCGCAGCGCAACTGTCG	900	Qy	1921	ACAAATCTTCTGCGGACCTGCGTCAATGGGGTGTGTGGACTGTCTATCATGTGTC	1980
Db	841		TTGTCGATCAGGATGATCTGGAAGAGATCAGGGGCTCGGCGCAGCGCAACTGTCG	900	Db	1921	ACAAATCTTCTGCGGACCTGCGTCAATGGGGTGTGTGGACTGTCTATCATGTGTC	1980
Qy	901		CCAGGCTCAAGGCGCGCATGCGGAGGAGATCTCGTGTGACCCCATGGCGATGTCCT	960	Qy	1981	GGCTCAAGACCTTTCGCGGCCCAAGGGCCCAATCACCACCAATGTACACCAATGTGGAC	2040
Db	901		CCAGGCTCAAGGCGCGCATGCGGAGGAGATCTCGTGTGACCCCATGGCGATGTCCT	960	Db	1981	GGCTCAAGACCTTTCGCGGCCCAAGGGCCCAATCACCACCAATGTACACCAATGTGGAC	2040
Qy	961		GCTTGCAGAAATCATGTTGGAATGGCGCTTTTCTGGATTCATCGACTGTGGCGGC	1020	Qy	2041	CAGGACCTCGTGGCTGGCAAGCGCCCCCGGGCGCTTCTCTGTGACACCATGCACTGC	2100
Db	961		GCTTGCAGAAATCATGTTGGAATGGCGCTTTTCTGGATTCATCGACTGTGGCGGC	1020	Db	2041	CAGGACCTCGTGGCTGGCAAGCGCCCCCGGGCGCTTCTCTGTGACACCATGCACTGC	2100
Qy	1021		TGGTGTGGGACCGCTATCAGGACATAGCGTTGGTACCCGTGATATTGCTGAAGAGC	1080	Qy	2101	GGAGCTCGGACCTTTTACTTGGTACAGGACATGCGGATGTCTATTCGGTGGCGCGCGG	2160
Db	1021		TGGTGTGGGACCGCTATCAGGACATAGCGTTGGTACCCGTGATATTGCTGAAGAGC	1080	Db	2101	GGAGCTCGGACCTTTTACTTGGTACAGGACATGCGGATGTCTATTCGGTGGCGCGCGG	2160
Qy	1081		TTGGGCGGAAATGCGGCTGACCGCTTCTCGTGTGCTTACGGTATCGCGCTCCCGATTGCG	1140	Qy	2161	GGCGACAGCAGGGGAGCTTACTCTCCCGAGCGCTCTCTTCTTGAAGGCTCTTCG	2220
Db	1081		TTGGGCGGAAATGCGGCTGACCGCTTCTCGTGTGCTTACGGTATCGCGCTCCCGATTGCG	1140	Db	2161	GGCGACAGCAGGGGAGCTTACTCTCCCGAGCGCTCTCTTCTTGAAGGCTCTTCG	2220
Qy	1141		AGCGATCGGCTTCTATCGGCTTCTTACGAGTCTTCTGAGTTTAAACAGACCAACAG	1200	Qy	2221	GGCGCTCCACTGCTGCCCCCTCGGGGACGCTGTGGGACATCTTTGGGCTGGCGTGTGC	2280
Db	1141		AGCGATCGGCTTCTATCGGCTTCTTACGAGTCTTCTGAGTTTAAACAGACCAACAG	1200	Db	2221	GGCGCTCCACTGCTGCCCCCTCGGGGACGCTGTGGGACATCTTTGGGCTGGCGTGTGC	2280
Qy	1201		GTTTCCCTTAGCGGATCAATTCGGCCCTCTCCCTCCCGCTTACTGTCG	1260	Qy	2281	ACCGAGGGTTCGGAAGGCGGTGGACTTTGTACCGCTCGAGTCTATGGAACCACTATG	2340
Db	1201		GTTTCCCTTAGCGGATCAATTCGGCCCTCTCCCTCCCGCTTACTGTCG	1260	Db	2281	ACCGAGGGTTCGGAAGGCGGTGGACTTTGTACCGCTCGAGTCTATGGAACCACTATG	2340
Qy	1261		CGAAGCGCTTGAATAAGGCGGCTGTCGTTTGTCTATATGTTTATTTCCACCATATG	1320	Qy	2341	CGGTCCCGCTTTCAGGACAACTCGTCCCTCCGSCCGTACCGAGACATTTCCAGGTG	2400
Db	1261		CGAAGCGCTTGAATAAGGCGGCTGTCGTTTGTCTATATGTTTATTTCCACCATATG	1320	Db	2341	CGGTCCCGCTTTCAGGACAACTCGTCCCTCCGSCCGTACCGAGACATTTCCAGGTG	2400
Qy	1321		CGGTCTTTTGGCAATGAGGCGCGGAAACCTGGCCCTGCTCTTGTGACGAGATTCCT	1380	Qy	2401	GCCCATCTACACGCCCTTACTGGTAGCGGCAAGAGCACTAAGGTGCGGCTGCGTATGCA	2460
Db	1321		CGGTCTTTTGGCAATGAGGCGCGGAAACCTGGCCCTGCTCTTGTGACGAGATTCCT	1380	Db	2401	GCCCATCTACACGCCCTTACTGGTAGCGGCAAGAGCACTAAGGTGCGGCTGCGTATGCA	2460
Qy	1381		AGGGTCTTTCCTCTCGCCAAAGGATGCAAGTCTGTTGAATGCTGTAAGGAGCA	1440	Qy	2461	GCCCAAGGGTATAGGTGCTTCTGAAACCGCTCGGTCCGCGCACCTTAGGTTCGGG	2520
Db	1381		AGGGTCTTTCCTCTCGCCAAAGGATGCAAGTCTGTTGAATGCTGTAAGGAGCA	1440	Db	2461	GCCCAAGGGTATAGGTGCTTCTGAAACCGCTCGGTCCGCGCACCTTAGGTTCGGG	2520
Qy	1441		GTTTCTCTGGAAGCTTCTTGAAGACAAACACGCTCTGTAGCGACCTTTTGCAGCAGCGG	1500	Qy	2521	GGCTATATGCTTAAGGCACATGTTATCGACCTTAAACATCAGAACCGGGGTAAAGCACATC	2580
Db	1441		GTTTCTCTGGAAGCTTCTTGAAGACAAACACGCTCTGTAGCGACCTTTTGCAGCAGCGG	1500	Db	2521	GGCTATATGCTTAAGGCACATGTTATCGACCTTAAACATCAGAACCGGGGTAAAGCACATC	2580
Qy	1501		AACCCCGACCTGCGGACAGTGTCTGCGGCCAAAGCCACGCTGATAGATACACCT	1560	Qy	2581	ACCACGGTGCCTCCCATACGTACTCCACCTATGGCAAGTTCCTTGGCGACGCTGGTTCG	2640
Db	1501		AACCCCGACCTGCGGACAGTGTCTGCGGCCAAAGCCACGCTGATAGATACACCT	1560	Db	2581	ACCACGGTGCCTCCCATACGTACTCCACCTATGGCAAGTTCCTTGGCGACGCTGGTTCG	2640
Qy	1561		GCAAGCGGCACAAACCGCTGCGGAGTGTGATGATGATGTTGGAAGAGTCAAA	1620	Qy	2641	TCTGGGGCGCTATGATCATATATGATGATGATGATGATGATGATGATGATGATGATGATG	2700
Db	1561		GCAAGCGGCACAAACCGCTGCGGAGTGTGATGATGATGATGATGATGATGATGATGATG	1620	Db	2641	TCTGGGGCGCTATGATCATATATGATGATGATGATGATGATGATGATGATGATGATGATG	2700
Qy	1621		TGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCAGAGGTACCCCATTTG	1680	Qy	2701	ATCCTGGGCTCGGACAGTCTTGGACCAAGCGGAGCGGCTGGAGCGGCTCGTCTG	2760
Db	1621		TGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCAGAGGTACCCCATTTG	1680	Db	2701	ATCCTGGGCTCGGACAGTCTTGGACCAAGCGGAGCGGCTGGAGCGGCTCGTCTG	2760

QY 2761 CTGGCCACCGCTACGGCTCCGGGATCGGTGACCGTGCACATCCAAACATCGAGGAGTG 2820  
DB 2761 CTGGCCACCGCTACGGCTCCGGGATCGGTGACCGTGCACATCCAAACATCGAGGAGTG 2820  
QY 2821 GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGGCCATCCCATCGAGACATC 2880  
DB 2821 GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGGCCATCCCATCGAGACATC 2880  
QY 2881 AAGGGGGGAGGACCTCATTTTTCTGCCATTCGAAGAAGATGTGATGAGCTCGCGGG 2940  
DB 2881 AAGGGGGGAGGACCTCATTTTTCTGCCATTCGAAGAAGATGTGATGAGCTCGCGGG 2940  
QY 2941 AAGCTGTCCGGCTCGACTCAATGTGTAGCATATACCGGGGCTTGATGTATCCGTC 3000  
DB 2941 AAGCTGTCCGGCTCGACTCAATGTGTAGCATATACCGGGGCTTGATGTATCCGTC 3000  
QY 3001 ATACCAACTAGCGGAGAGCTGATTCGTGTAGCAATACCGAGGCTTAATGACGGGCTTTAC 3060  
DB 3001 ATACCAACTAGCGGAGAGCTGATTCGTGTAGCAATACCGAGGCTTAATGACGGGCTTTAC 3060  
QY 3061 GCGGATTTGCACTCAGTGTGACTGCAATATGTCACCGACAGCTGACATTCAGC 3120  
DB 3061 GCGGATTTGCACTCAGTGTGACTGCAATATGTCACCGACAGCTGACATTCAGC 3120  
QY 3121 CTGGACCCGACCTTACCAATTTAGAGAGAGCGACCGTGCACAGACGCGGTTCACGCTCG 3180  
DB 3121 CTGGACCCGACCTTACCAATTTAGAGAGAGCGACCGTGCACAGACGCGGTTCACGCTCG 3180  
QY 3181 CAGCGGCGAGCAGGACTGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA 3240  
DB 3181 CAGCGGCGAGCAGGACTGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA 3240  
QY 3241 GAAAGGCGCTCCGGCATTTGCAATTCCTCGGTTCTGTGCGAGTGTATGACGCGGCTGT 3300  
DB 3241 GAAAGGCGCTCCGGCATTTGCAATTCCTCGGTTCTGTGCGAGTGTATGACGCGGCTGT 3300  
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DB 3301 GCTTGTGTACGAGCTCAAGCGCGGAGACCTCAAGTTAGGTTGCGGCTTACCTAAACACA 3360  
QY 3361 CCAGGTTGCGGCTGCGAGGACCTGAGTGTGAGTGTGAGGAGGCTTTACAGGCTC 3420  
DB 3361 CCAGGTTGCGGCTGCGAGGACCTGAGTGTGAGTGTGAGGAGGCTTTACAGGCTC 3420  
QY 3421 ACCACATAGACGCGCAATTTCTGTCCAGACTAAGCAGGAGGAGACAACTTCCCTTAC 3480  
DB 3421 ACCACATAGACGCGCAATTTCTGTCCAGACTAAGCAGGAGGAGACAACTTCCCTTAC 3480  
QY 3481 CTGGTAGCATACGAGGCTACCGGTGCGCCAGGCTCAGGCTCCACCTCCATCGTGGGAC 3540  
DB 3481 CTGGTAGCATACGAGGCTACCGGTGCGCCAGGCTCAGGCTCCACCTCCATCGTGGGAC 3540  
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DB 3541 CAATGTGGAGTGTCTCATACGCTAAGGCTACGCTGACGCGGCAAGCGCCCTGTG 3600  
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DB 3601 TATAGGCTGGAGCGGTTCAAAACGAGGTTACTACCAACACCCCAATAACCAATATC 3660  
QY 3661 ATGGCATGATGTCCGCTGACCTGGAGGTGTGTACAGGACCTGGGTGCTGGAGCGGA 3720  
DB 3661 ATGGCATGATGTCCGCTGACCTGGAGGTGTGTACAGGACCTGGGTGCTGGAGCGGA 3720  
QY 3721 GTCCTAGCAGCTGTGGCGGCTATTTGCTGTACACAGGAGCGGTGTGATTTGGGCGAG 3780  
DB 3721 GTCCTAGCAGCTGTGGCGGCTATTTGCTGTGTGACAAACAGGAGCGGTGTGATTTGGGCGAG 3780  
QY 3781 ATCATCTTGTCCGAAAGCGGCTCATTTCCCGACAGGGAAGTCCCTTTACCGGAGTTC 3840  
DB 3781 ATCATCTTGTCCGAAAGCGGCTCATTTCCCGACAGGGAAGTCCCTTTTACCGGAGTTC 3840

QY 3841 GATGAGATGGAAGAGTGCCTCACAACCTCCCTTATCATCGAACAGGGAATGAGCTCGCC 3900  
DB 3841 GATGAGATGGAAGAGTGCCTCACAACCTCCCTTATCATCGAACAGGGAATGAGCTCGCC 3900  
QY 3901 GAAACAATTCAAAACAGAGCAATCGGGTTGTGCAAAACAGCCACCAAGCAAGCGGAGGCT 3960  
DB 3901 GAAACAATTCAAAACAGAGCAATCGGGTTGTGCAAAACAGCCACCAAGCAAGCGGAGGCT 3960  
QY 3961 GCTGTCTCCGCTGGTGGATCCAAAGTGGCGGACCTCTGAAAGCCCTTCTGGCGGAGCATATG 4020  
DB 3961 GCTGTCTCCGCTGGTGGATCCAAAGTGGCGGACCTCTGAAAGCCCTTCTGGCGGAGCATATG 4020  
QY 4021 TGGAAATTTTCATCAGCGGGATACAATATTTAGCAGGCTGTCTCCACTCTGCTGCAACCCC 4080  
DB 4021 TGGAAATTTTCATCAGCGGGATACAATATTTAGCAGGCTGTCTCCACTCTGCTGCAACCCC 4080  
QY 4081 GCGATAGCATCTCATGTGCAATTCACGCTCTATCACCAGCCGCTCACCACCCCAACAT 4140  
DB 4081 GCGATAGCATCTCATGTGCAATTCACGCTCTATCACCAGCCGCTCACCACCCCAACAT 4140  
QY 4141 ACCCTCTCTTTTAAACATCTCGGGGGATGGTGGCGGCCCAACTTGTCTCTCCAGCGCT 4200  
DB 4141 ACCCTCTCTTTTAAACATCTCGGGGGATGGTGGCGGCCCAACTTGTCTCTCCAGCGCT 4200  
QY 4201 GCTTCTGCTTTCTGTAAGCGCGGATCGCTGAGCGGCTGTGGCAGCATAGGCTTGGG 4260  
DB 4201 GCTTCTGCTTTCTGTAAGCGCGGATCGCTGAGCGGCTGTGGCAGCATAGGCTTGGG 4260  
QY 4261 AAGGTGCTTTGTGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGCGCTCGTGGCC 4320  
DB 4261 AAGGTGCTTTGTGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGCGCTCGTGGCC 4320  
QY 4321 TTTAAGTTCATGAGCGGGAGATGCCCTCACAAGGAGACCTGGTTAACTATCCTCTGCT 4380  
DB 4321 TTTAAGTTCATGAGCGGGAGATGCCCTCACAAGGAGACCTGGTTAACTATCCTCTGCT 4380  
QY 4381 ATCTCTCTCCCTGCGGCTTAGTCTGCGGGTCTGTGCGCAGCGATACCTGCTGGCAC 4440  
DB 4381 ATCTCTCTCCCTGCGGCTTAGTCTGCGGGTCTGTGCGCAGCGATACCTGCTGGCAC 4440  
QY 4441 GTGGGCCAGGGGAGGGGCTGTGCAAGTGAACCGGCTGATAGCGCTTCTGCTTCGCGG 4500  
DB 4441 GTGGGCCAGGGGAGGGGCTGTGCAAGTGAACCGGCTGATAGCGCTTCTGCTTCGCGG 4500  
QY 4501 GGTAAACACGCTCTCCCGACGACTATGTGCTGAGAGCGACGCTGAGCAGCTGTCACT 4560  
DB 4501 GGTAAACACGCTCTCCCGACGACTATGTGCTGAGAGCGACGCTGAGCAGCTGTCACT 4560  
QY 4561 CAGATCTCTCTAGTCTTACCATCAGCTCAGCTGCTGAAGGCTTCAACAGTGAATCAAC 4620  
DB 4561 CAGATCTCTCTAGTCTTACCATCAGCTCAGCTGCTGAAGGCTTCAACAGTGAATCAAC 4620  
QY 4621 GAGGACTGTCTCAGCGCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATTTGATATGC 4680  
DB 4621 GAGGACTGTCTCAGCGCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATTTGATATGC 4680  
QY 4681 ACGGTGTGATGATTTCAAGACTTCCAGCTCAGTCCAGCTCCTGCGCGCATTCGCGGA 4740  
DB 4681 ACGGTGTGATGATTTCAAGACTTCCAGCTCAGTCCAGCTCCTGCGCGCATTCGCGGA 4740  
QY 4741 GTCCCTCTCTCTCATGTCAAGCTGGGTCAAGGAGTCTGGCGGGGCGAGCGCATCATG 4800  
DB 4741 GTCCCTCTCTCTCATGTCAAGCTGGGTCAAGGAGTCTGGCGGGGCGAGCGCATCATG 4800  
QY 4801 CAAACCACTTCCCATGTGGAGCAGATCAACCGGACATGTGAACAAACGGTTCCTATGAG 4860  
DB 4801 CAAACCACTTCCCATGTGGAGCAGATCAACCGGACATGTGAACAAACGGTTCCTATGAG 4860  
QY 4861 ATCGTGGGCGCTTAGGACCTGTAGTAAACGCTGCAATTTCCCATTAACGCGTAC 4920  
DB 4861 ATCGTGGGCGCTTAGGACCTGTAGTAAACGCTGCAATTTCCCATTAACGCGTAC 4920  
QY 4921 ACCACGGGCGCTGCAAGCGCTTCCCGGCGCCAAATTTCTTAGGGGCTGTGGCGGGTG 4980

Db	4921	ACACGGGCCCCCTGACGCGCTCCCGGCGCCAAATATCTAGGGCGCTGTGGCGGTG	4980	6001	ACAGCGCCCTGATCAGCCATGCGCTGCGGAGGAAACCAAGCTGCCATCAATGCACCTG	6060	
Qy	4981	GCTGCTAGGAGTACGTGAGGTTACCGGGTGGGGATTTCCATACGTGTGAGGGCATG	5040	Qy	6061	AGCAACTCTTTCTCGTCCGTCACCAACAATTTGCTATGTCTACAACTCTCGCAGCGCAAGC	6120
Db	4981	GCTGCTAGGAGTACGTGAGGTTACCGGGTGGGGATTTCCATACGTGTGAGGGCATG	5040	Db	6061	AGCAACTCTTTCTCGTCCGTCACCAACAATTTGCTATGTCTACAACTCTCGCAGCGCAAGC	6120
Qy	5041	ACCATGACAAAGTAAAGTGGCGGTGACGTTCCGGCCCCCGAAATTTCTACAGAAAGT	5100	Qy	6121	CTGCGCGAGAAAGAGTCACTTTGACAGACTGCGAGTCTCTGACGACCACTACCGGGAC	6180
Db	5041	ACCATGACAAAGTAAAGTGGCGGTGACGTTCCGGCCCCCGAAATTTCTACAGAAAGT	5100	Db	6121	CTGCGCGAGAAAGTCACTTTGACAGACTGCGAGTCTCTGACGACCACTACCGGGAC	6180
Qy	5101	GATGGGTTGGGTTGACAGGTACGCTCCAGCGTGCAAAACCCCTCTACCGGAGGAGT	5160	Qy	6181	GTGCTCAAGGAGTGAAGCGAGGCTCCACAGTTTAAAGCTTAACTTCTATCCGTGGAG	6240
Db	5101	GATGGGTTGGGTTGACAGGTACGCTCCAGCGTGCAAAACCCCTCTACCGGAGGAGT	5160	Db	6181	GTGCTCAAGGAGTGAAGCGAGGCTCCACAGTTTAAAGCTTAACTTCTATCCGTGGAG	6240
Qy	5161	ACATTCCTGGTGGGCTCAATCAATACCTGTTGGTTCACAGTCCCATCGAGCCCGAA	5220	Qy	6241	GAAGCTGTAAAGCTGACGCCCCACATTCGGCCAGATCTAAATTTGGCTATGGGCAAG	6300
Db	5161	ACATTCCTGGTGGGCTCAATCAATACCTGTTGGTTCACAGTCCCATCGAGCCCGAA	5220	Db	6241	GAAGCTGTAAAGCTGACGCCCCACATTCGGCCAGATCTAAATTTGGCTATGGGCAAG	6300
Qy	5221	CGGAGTACGAGTCACTTCCATGCTCACCGACCCCTCCACATTAAGCGGAGAGC	5280	Qy	6301	GACGTCGGAACTTATCCAGCAAGCGCTTAAACCATCGCTCCGTGTGGAAGGACTT	6360
Db	5221	CGGAGTACGAGTCACTTCCATGCTCACCGACCCCTCCACATTAAGCGGAGAGC	5280	Db	6301	GACGTCGGAACTTATCCAGCAAGCGCTTAAACCATCGCTCCGTGTGGAAGGACTT	6360
Qy	5281	GCTAAGCTAGGCTGGCGAGGGATCTCCCCCTCTTGGCCAGCTCATCAGCTAGCCAG	5340	Qy	6361	CTGGAAGACACTGAGACCAATTAACACCACTCATGGCAAAATAGGTTTCTG	6420
Db	5281	GCTAAGCTAGGCTGGCGAGGGATCTCCCCCTCTTGGCCAGCTCATCAGCTAGCCAG	5340	Db	6361	CTGGAAGACACTGAGACCAATTAACACCACTCATGGCAAAATAGGTTTCTG	6420
Qy	5341	CTGCTGCGCTTCTTTGAGGAAAGTAAATTTGGACTCTTTGAGCGCTTCAAGCGAGGAGT	5400	Qy	6421	GTCCAAACAGAGAGGCGGCGCAAGCCAGCTCGCTTATCGTATTTCCAGATTTGGG	6480
Db	5341	CTGCTGCGCTTCTTTGAGGAAAGTAAATTTGGACTCTTTGAGCGCTTCAAGCGAGGAGT	5400	Db	6421	GTCCAAACAGAGAGGCGGCGCAAGCCAGCTCGCTTATCGTATTTCCAGATTTGGG	6480
Qy	5401	CTCATGAGGCAACCTCTGCGCGCAGGAGTGGCGGGAACATCAACCGCTGGAG	5460	Qy	6481	GTTCTGTGTGCGAGAAATGGCCCTTACGATGTGTCTCCACCTCTCCCTCAGGCGGT	6540
Db	5401	CTCATGAGGCAACCTCTGCGCGCAGGAGTGGCGGGAACATCAACCGCTGGAG	5460	Db	6481	GTTCTGTGTGCGAGAAATGGCCCTTACGATGTGTCTCCACCTCTCCCTCAGGCGGT	6540
Qy	5461	TCAGAAATAGGTAGTAAATTTGGACTCTTTGAGCGCTTCAAGCGAGGAGT	5520	Qy	6541	ATGGCTCTTCAACCGATTCCTCTCGGACAGCGGTTCAGTTCTCTGTTGAAT	6600
Db	5461	TCAGAAATAGGTAGTAAATTTGGACTCTTTGAGCGCTTCAAGCGAGGAGT	5520	Db	6541	ATGGCTCTTCAACCGATTCCTCTCGGACAGCGGTTCAGTTCTCTGTTGAAT	6600
Qy	5521	AGGAAAGTATCGTTCCGGCGGAGATCTCGGAGGTCAGGAAATTTCCCTCGAGCAT	5580	Qy	6601	GCCTGGAAGCGAGAAATGCCCTATGGCTTCGCATATGACACCCCTGTTTGAATCA	6660
Db	5521	AGGAAAGTATCGTTCCGGCGGAGATCTCGGAGGTCAGGAAATTTCCCTCGAGCAT	5580	Db	6601	GCCTGGAAGCGAGAAATGCCCTATGGCTTCGCATATGACACCCCTGTTTGAATCA	6660
Qy	5581	CCCATATGGCACCGCGGATTAACACCTCTCTAGTCTGCAAGGAGCCCGGAC	5640	Qy	6661	ACGGTCACTGAGATGACATCCGTGTGAGGAGTCAATCTACCAATGTTGACTGCGC	6720
Db	5581	CCCATATGGCACCGCGGATTAACACCTCTCTAGTCTGCAAGGAGCCCGGAC	5640	Db	6661	ACGGTCACTGAGATGACATCCGTGTGAGGAGTCAATCTACCAATGTTGACTGCGC	6720
Qy	5641	TACGTCCTCCAGTGGTACACGGGTGTCCATTCGCGCTGCAAGGAGCCCTCGATACCA	5700	Qy	6721	CCGAGCCAGACAGGCGCTACAGAGCGGCTTTACATCGGGGGCCCCCTG	6780
Db	5641	TACGTCCTCCAGTGGTACACGGGTGTCCATTCGCGCTGCAAGGAGCCCTCGATACCA	5700	Db	6721	CCGAGCCAGACAGGCGCTACAGAGCGGCTTTACATCGGGGGCCCCCTG	6780
Qy	5701	CCTCCAGAGGAGAGAGCGGTTGCTGTACAAATCTACCGTCTTCTGCTTGGCG	5760	Qy	6781	ACTAAATTTAAAGGCGAGAACTGCGGCTATCGCGGTGCGCGCGAGCGGTACTGACG	6840
Db	5701	CCTCCAGAGGAGAGAGCGGTTGCTGTACAAATCTACCGTCTTCTGCTTGGCG	5760	Db	6781	ACTAAATTTAAAGGCGAGAACTGCGGCTATCGCGGTGCGCGCGAGCGGTACTGACG	6840
Qy	5761	GAGCTCGGCAAGAGACTTCGCGAGCTCGAAATCGCGGCTCGACAGCGGCGGCA	5820	Qy	6841	ACCAGCTCGGTAATACCTTACATGTTACTTGAAGCGCGCTGCGGCTGTCGAGCTGCG	6900
Db	5761	GAGCTCGGCAAGAGACTTCGCGAGCTTCGAAATCGCGGCTCGACAGCGGCGGCA	5820	Db	6841	ACCAGCTCGGTAATACCTTACATGTTACTTGAAGCGCGCTGCGGCTGTCGAGCTGCG	6900
Qy	5821	ACGGCTCTCTGACAGGCTTCGAGACGCGGAGCGGGATCCGAGTTGAGTCGAT	5880	Qy	6901	AGCTCCAGACTGACGATGCTGATGCGGAGACCTTGTGCTTATCTGTGAAAGC	6960
Db	5821	ACGGCTCTCTGACAGGCTTCGAGACGCGGAGCGGGATCCGAGTTGAGTCGAT	5880	Db	6901	AGCTCCAGACTGACGATGCTGATGCGGAGACCTTGTGCTTATCTGTGAAAGC	6960
Qy	5881	TCCTCCATGCCCCCTTACGGGAGCGGGGATCCGATCTCAGGAGCGGCTTGG	5940	Qy	7021	TCTGCCCTCTGGGAGCCGCCAAACCAAGAGTGGAGTTGATTAACATATGC	7080
Db	5881	TCCTCCATGCCCCCTTACGGGAGCGGGGATCCGATCTCAGGAGCGGCTTGG	5940	Db	7021	TCTGCCCTCTGGGAGCCGCCAAACCAAGAGTGGAGTTGATTAACATATGC	7080
Qy	5941	TCTACCGTAAAGGAGGCTAGTACAGGAGCTGCTGCTGCTGCTGCTTACACATG	6000	Qy	7081	TCCTCCATGTTGTCAGTCCGCGACGATGCTGCGCAAAAGGGTGTACTATCTACCCGT	7140
Db	5941	TCTACCGTAAAGGAGGCTAGTACAGGAGCTGCTGCTGCTGCTGCTTACACATG	6000	Db	7081	TCCTCCATGTTGTCAGTCCGCGACGATGCTGCGCAAAAGGGTGTACTATCTACCCGT	7140
Qy	6001	ACAGCGCCCTGATCACGCCATGCGCTGCGGAGGAAACCAAGCTGCCCCATCAATGCAC	6060	Qy	7140	TCCTCCATGTTGTCAGTCCGCGACGATGCTGCGCAAAAGGGTGTACTATCTACCCGT	7140
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[illegible]

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Qy	5281	GCTAAGCGTAGGCTGGCGAGGGATCTCCCCCTCTTGCCGAGCTCATCAGCTAGCCAG	5340	Qy	6361	CTGGAAGACACTGAGACACCAATTTGACACCACTATCGCAAAAATAATGAGTTTTCTGC	6420
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Qy	5341	CTGCTGGGCGCTTCTTGGAAGCAACATGCACTACCCGTCATGACTCCCGGACGCTGAC	5400	Qy	6421	GTCCAAACAGAGAAAGGGGGCGCAAGCAGCTCGCTTATCGTATTTCCAGATTTGGGG	6480
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Db	5401	CTCATCGAGGCCAACCTCTGTGGCGCAGGAGATGGCGGGAACATCAACCCGCTGGAG	5460	Db	6481	GTTCGCTGTGCGAGAAATGCCCCCTTTACGATGTGTCTCCACCTCCCTCAGGCGGTG	6540
Qy	5461	TCAGAAATAAGGTAGTAATTTTGGACTCTTTGAGGAGCAATGCACTACCCGTCATGACTCCCGGACGCTGAC	5520	Qy	6541	ATGGGCTCTTTCATACGGATTCCTCTCTGGACAGCGGTGAGTTCTCTGTGTAAT	6600
Db	5461	TCAGAAATAAGGTAGTAATTTTGGACTCTTTGAGGAGCAATGCACTACCCGTCATGACTCCCGGACGCTGAC	5520	Db	6541	ATGGGCTCTTTCATACGGATTCCTCTCTGGACAGCGGTGAGTTCTCTGTGTAAT	6600
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Db	5521	AGGGAAGTATCCGTTCCGGCGGAGATCCCTCGGAGGTCCAGAAATTCCTCTCGAGCGATG	5580	Db	6601	GCTCGAAGCGAAGAAATGCCCCCTATGGGCTTCGATATGACACCGGCTGTTTGACTCA	6660
Qy	5581	CCCATATGGGCAACCCCGGATTAACACCCTCCAATGCTTAGAGTCTTGGAAGCAACCCGAC	5640	Qy	6661	ACGGTCACCTGAGAATGACATCCGTTGAGGAGTCAATCTACCAATGTTGACTTTGGGC	6720
Db	5581	CCCATATGGGCAACCCCGGATTAACACCCTCCAATGCTTAGAGTCTTGGAAGCAACCCGAC	5640	Db	6661	ACGGTCACCTGAGAATGACATCCGTTGAGGAGTCAATCTACCAATGTTGACTTTGGGC	6720
Qy	5641	TAGCTCCCTCAGTGTGACACGGGTGTCATTTGCCGCTGCCAAGGCCCTCCGATACCA	5700	Qy	6721	CCCGAAGCCAGACAGGCCATAAGTCGCTCACAGAGCGGCTTTACATCGGGGGCCCCCTG	6780
Db	5641	TAGCTCCCTCAGTGTGACACGGGTGTCATTTGCCGCTGCCAAGGCCCTCCGATACCA	5700	Db	6721	CCCGAAGCCAGACAGGCCATAAGTCGCTCACAGAGCGGCTTTACATCGGGGGCCCCCTG	6780
Qy	5701	CTTCCACGAGGAGGAGCGGTTGCTGTCAAGATCTACCGTGTCTTCTGCTTTGGG	5760	Qy	6781	ACTAATTTCTAAGGGCAGAACTGCGGCTATCGCGGTGCGGCGGAGCGGTGACTGACG	6840
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Qy	5761	GAGCTGCCACAAAGACCTTGGCAGCTCCGAATCGTCGCGCGTCCGACGCGGCAACGGCA	5820	Qy	6841	ACAGCTGCGGTAATACCTCATGTTTGAAGCGCGCTGCGGCGGTGCGAGCTGCG	6900
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Qy	5821	AGGCTCTCTGACACAGCCCTCCGAGGACGGGACCGGGATCCGACGTTGATCGTAC	5880	Qy	6901	AAGCTCCAGGACTGACGAGTGTCTGATGCGGAGACGACCTTGTCTGTTATCTGTGAAAGC	6960
Db	5821	AGGCTCTCTGACACAGCCCTCCGAGGACGGGACCGGGATCCGACGTTGATCGTAC	5880	Db	6901	AAGCTCCAGGACTGACGAGTGTCTGATGCGGAGACGACCTTGTCTGTTATCTGTGAAAGC	6960
Qy	5881	TCTCTCATGCCCTTTGAGGGGAGCGGGGATCCCGATCTCAGCGACGCGGTCTTGG	5940	Qy	6961	GCGGGACCCAGAGGACGAGGGGAGCTTACGGGCTTACGGAGGCTATGACTAGTAC	7020
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Db	5941	TCTACCGTAAGCGAGGAGGCTAGTGAAGAGCTGTGTGTGCTCGATGTCCTACATGG	6000	Db	7021	TCTGCCCCCTGGGACCCGCCAAACCCAGAAATACGACTTGGAGTTGATAACATCATGC	7080
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Qy	6181	GTGCTCAAGGAGATGAAGGAGAGGCGTCCACAGTTAAGGCTAACTTCTATCCGTGGAG	6240	Qy	7261	ACTCAITTTCTTCCATCTTCTAGCTCAGGAAACAACTTGAAGAGCCCTAGATTGTGAG	7320
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Qy	6241	GAAGCTGTAAAGCTGACGCCCCCACTTCGSCCAGATCTAAATTTGGCTATGGGCAAG	6300	Qy	7321	ATCTAGGGGCTGTTACTCCATTGAGCCACTTGACCTACTCTCAGATCAATCAACGACTC	7380
Db	6241	GAAGCTGTAAAGCTGACGCCCCCACTTCGSCCAGATCTAAATTTGGCTATGGGCAAG	6300	Db	7321	ATCTAGGGGCTGTTACTCCATTGAGCCACTTGACCTACTCTCAGATCAATCAACGACTC	7380
Qy	6301	GAGTCGCGAACCTATCCAGCAAGGCGTTTAAACCATTCGCTCCGTGTGGAAGGACTTG	6360	Qy	7381	CATGGCTTAGCGCAATTTTCACTCCATAGTACTCTCCAGGTGAGATCAATAGGGTGGCT	7440
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 ORGANISM Hepatitis C virus replicon 1377/NS3-3'UTR  
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 TITLE Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell line  
 JOURNAL Science 285 (5424), 110-113 (1999)  
 MEDLINE 93321193  
 PUBMED 10390360  
 REFERENCE 2 (bases 1 to 7989)  
 AUTHORS Bartenschlager, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-MAY-1999) Bartenschlager R., Institute for Virology, Johannes Gutenberg - University Mainz, Obere Zahlbacher Strasse 67, 55131 Mainz, GERMANY  
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VERSION AR406042.1 GI:40155169  
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SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 8001)  
AUTHORS Bartenschlager,R.  
TITLE Hepatitis C virus culture system  
JOURNAL Patent: US 6630343-A 7 07-OCT-2003;

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Qy	61	TCTTCACGCAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGACAGCTCCAGGAC 120
Db	61	TCTTCACGCAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGACAGCTCCAGGAC 120
Qy	121	CCCCCTCCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAG 180
Db	121	CCCCCTCCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAG 180
Qy	181	GACGACCGGTCTTCTTGGATCAACCCGCTCAATGCTGGAGATTGGGGGTGCCCCC 240
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Qy	241	GCAGACTCTAGCCGAGTAGTGTGGGTGCGGAAGGCTTGTGCTACTGCTGATAGG 300
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Qy	301	GTGCTTGCAGTGCCTCCCGGAGGTCTCGTAGACCGGTGCACCATGAGCAGAAATCCTAAAC 360
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Db	361	CTCAAGAAACCAAACTAAACCAACCGGCGCGCCATGATTGAACAAGATGGATTGC 420
Qy	409	ACGAGAGTTCTCGGCGCGTCTGGGTGGAGAGGCTATTTCGGCTATGACTTGGGCACACAGA 468
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DEFINITION Sequence 3, from Patent EP1043399.
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VERSION AX036254.1 GI:11225870
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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AUTHORS Bartenschlager,R.D.
TITLE Hepatitis c virus cell culture system
JOURNAL Patent: EP 1043399-A 3 11-OCT-2000;
BARTENSCHLAGER RALF DR (DE)
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Lohmann, V., Korner, F., Koch, J., Herian, U., Theilmann, L. and  
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TITLE  
Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell  
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Science 285 (5424), 110-113 (1999)  
MEDLINE  
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AUTHORS  
Bartenschlager, R.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (26-MAY-1999) Bartenschlager R., Institute for Virology,  
Johannes Gutenberg - University Mainz, Obere Zahlbacher Strasse 67,  
55131 Mainz, GERMANY

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ORGANISM Unknown.
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AUTHORS Bartenschlager,R.
TITLE Hepatitis C virus culture system
JOURNAL Patent: US 6630343-A 22 07-OCT-2003;
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VERSION AX036257.1 GI:11225873
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SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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AUTHORS Bartenschlager R.D.
TITLE Hepatitis C virus cell culture system
JOURNAL Patent: EP 1043399-A 6 11-OCT-2000;
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ORGANISM	Unknown.		
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AUTHORS	1 (bases 1 to 8001)		
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JOURNAL	Hepatitis C virus culture system		
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Best Local Similarity	99.7%;	Pred. No. 0;	
Matches 7973;	Conservative	0; Mismatches	16; Indels 12; Gaps 1;
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Db	1	GCAGCCCCCGATTGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGGAATCTACTG	60
QY	61	TCTTCACGCAGAAAGCGTCTAGCCATGGGTTAGTATGATGATGCTGTCGTCAGCCCTCAGGAC	120
Db	61	TCTTCACGCAGAAAGCGTCTAGCCATGGGTTAGTATGATGATGCTGTCGTCAGCCCTCAGGAC	120
QY	121	CCCCCTCCCGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAG	180
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QY	241	GGGAGACTGCTAGCCGAGTAGTGTGGTTCGCGAAAGCCCTTGTGGTACTGCCTGATAGG	300
Db	241	GGGAGACTGCTAGCCGAGTAGTGTGGTTCGCGAAAGCCCTTGTGGTACTGCCTGATAGG	300
QY	301	GTGCTTGGAGTGCCCGGGAGGCTCTGATAGCCGTGCACCATGAGCAGCAATCCTAAAC	360
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QY	361	CTCAAGAAAAACCAAA-----GGGCGCGCATGATTGAACAAGATGGATTGC	408
Db	361	CTCAAGAAAAACCAAGTAAACCAACGGCGCGCATGATTGAACAAGATGGATTGC	420

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QY		3229	GTGACTCGAGGAAACGGGCCCTCGGGCATGTTTCGATTCTCGTTCGAGTGCCTAT	3288
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QY		3289	GACGCGGCTGTCTGTGTGACGAGCTACGCCCGCCGACCTCAGTTAGTTTGGGCT	3348
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QY	4189	CCTCCACAGCGTCTTCTGCTTTCTGTAGCGCGGCATCGCTGGAGCGGTGTGGCAGC	4248
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QY	4609	CAGTGGATCAACAGGAGTGTCTCCACGCCATGTCTCCGCTCGTGGCTAAGAGATGTTTGG	4668
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QY	4669	GATTGGATATGACGGTGTGACTGATTTTCAAGCTTGGCTCCAGTCCCAAGCTCTGCCG	4728
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QY	4729	CGATTGCCGGAGTCCCTTCTTCTCATGTCAACGTGGGTACAGGGAGTCTGGCGGGC	4788
Db	4741	CGATTGCCGGAGTCCCTTCTTCTCATGTCAACGTGGGTACAGGGAGTCTGGCGGGC	4800



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AX036261

LOCUS AX036261 8001 bp DNA linear PAT 16-NOV-2000  
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ACCESSION AX036261  
VERSION AX036261.1 GI:11225877  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
KEYWORDS Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1  
AUTHORS Bartenschlager R.D.  
TITLE Hepatitis C virus cell culture system  
JOURNAL Patent: EP 1043399-A 10 11-OCT-2000;  
BARTENSCHLAGER RALF DR (DE)  
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## ORIGIN

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QY	6109	CGCAGCGCAAGCTTCGGGCAGAAAGGTCACTTTGACAGACTGCAGSTCTCTGGACGAC	6168
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Db 7321 CTAGATTGTGAGACTACGGGGCCCTGTTACTTCCATTGAGCCACTTGACTACCTACCTCAGATC 7380

Qy 7369 ATTCAACGACTCCATGCGCTTAGCGGATTTTCACTCCATAGTTACTCTCCAGGTGAGATC 7428

Db 7381 ATTCAACGACTCCATGCGCTTAGCGGATTTTCACTCCATAGTTACTCTCCAGGTGAGATC 7440

Qy 7429 AATAGGTTGGCTTCACTCCCTCAGGAACCTTGGGCTACCGCCCTTGGAGTCTGGAGACAT 7488

Db 7441 AATAGGTTGGCTTCACTCCCTCAGGAACCTTGGGCTACCGCCCTTGGAGTCTGGAGACAT 7500

Qy 7489 CGGGCCAGAGTGTCCCGCTAGGCTACTCTCCAGGGGGGAGGGCTGCCACTTGTGGC 7548

Db 7501 CGGGCCAGAGTGTCCCGCTAGGCTACTCTCCAGGGGGGAGGGCTGCCACTTGTGGC 7560

Qy 7549 AAGTACCTCTTCAACTGGGAGTAAGGACCAAGCTCAACTCACTCAATCCCGGCTGGC 7608

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Qy 7669 AGCTGTCTGTCGCGCCGACCCCGCTGGTTCTATGTTGCTACTCTCTACTTCTGTAGG 7728

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Qy 7729 GTAGGATCTACTACTCCCAACCGATGAACGGGAGCTAAACCTCAGGCCAATAGG 7788

Db 7741 GTAGGATCTACTACTCCCAACCGATGAACGGGAGCTAAACCTCAGGCCAATAGG 7800

Qy 7789 CCATCTGTTTTTTCCTT 7848

Db 7801 CCATCTGTTTTTTCCTT 7860

Qy 7849 TTTTCTCTTTTTTTTTTCTTTTTTTTCTTTTTTCTTTTTTCTTTTTTCTTTTTTCTTTAGC 7908

Db 7861 TTTTCTCTTTTTTTTTTCTTTTTTTTCTTTTTTCTTTTTTCTTTTTTCTTTTTTCTTTAGC 7920

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Db 7981 TGGCTCTCTGAGATCAAGT 8001

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DEFINITION Sequence 2 from Patent WO03091439.  
ACCESSION AX937622  
VERSION AX937622.1 GI:40713673  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1  
AUTHORS Duggal,R.A., Patick,A.K., Zhang,J.A. and Zhao,W.A.  
TITLE Reporter-selectable hepatitis c virus replicon  
JOURNAL Patent: WO 03091439-A 2 06-NOV-2003;  
PRIZER INC. (US)  
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ORIGIN

Query Match 95.2%; Score 7611.8; DB 6; Length 12305;  
Best local Similarity 100.0%; Pred. No. 0;  
Matches 7613; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1370 GGGCGCGCCATGATTGACACAGATGATTCACGACGAGTTCCTCGCGCGCTTGGTGGAG 1429

Qy 438 AGGCTATTTCGGCTATGACTGGGCACACACAGACAAATCGGCTGCTCTGATGCGCGCTTTC 497

Db 1430 AGGCTATTTCGGCTATGACTGGGCACACACAGACAAATCGGCTGCTCTGATGCGCGCTTTC 1489

Qy 498 CGGCTGTACGCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGTTGCCCTG 557

Db 1490 CGGCTGTACGCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGTTGCCCTG 1549

Qy 558 AATGAACATCGACGACGAGCGCGGCTATCGTGTGCTGGCAGACGCGGCGTTCCCTTGC 617

Db 1550 AATGAACATCGACGAGCGCGGCTATCGTGTGCTGGCAGACGCGGCGTTCCCTTGC 1609

Qy 618 GCAGCTGTCTCGACGCTTGTCTACCTTGTCTCTCTCCGCGAGAAAGTATCCATCATGGCT 677

Db 1610 GCAGCTGTCTCGACGCTTGTCTACCTTGTCTCTCTCCGCGAGAAAGTATCCATCATGGCT 1669

Qy 678 CGGGGCGAGGATCTCTGTCTATCTCACTTGTCTCTCTCCGCGAGAAAGTATCCATCATGGCT 737

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Db	4610	TCAAAACAGGTTACTACCAACACACCCCATAAACCAATACATCATGSCATGTCGGC	4669
QY	3678	TGACCTGGAGGTGCTCAAGAGACCTGGGTGCTGGTAGGCGGAGTCCCTAGCAGCTCGGC	3737
Db	4670	TGACCTGGAGGTGCTCAAGAGACCTGGGTGCTGGTAGGCGGAGTCCCTAGCAGCTCGGC	4729
QY	3738	CGGCTATGCTGACAAACAGGAGCGTGGTCACTGTGGGCGAGATCACTTTGCCGAAA	3797
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QY	3798	GCGGCGCATCATTCGCGACAGGGAAGTCTCTTTACCGGAGTTCGATGAGATGGAAGTG	3857
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QY	3858	CGGCTCACAGCTCCCTTACATCGAAACAGGGAATGCAAGTCCGCGAAACAAATTCAGAA	3917
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QY	3918	GGCAATCGGGTTGCTCAAAACAGCCACCAAGCAAGCGAGGCTGCTCCCGTGGTGA	3977
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QY	3978	ATCCAGTGGGACCCCTCGAAGCTTCTGGGCGAAGCATATGTGAAATTCATCAGCGG	4037
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QY	4038	GATCAAAATTTAGCAGGCTTGTCCACTCTGCTGCGCAACCCCGGATAGCATCACTGAT	4097
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QY	4098	GGCATTCAGGCTCTATCACCAGCGGCTCACCAACCAACATACCTCTCTTTAAAT	4157
Db	5090	GGCATTCAGGCTCTATCACCAGCGGCTCACCAACCAACATACCTCTCTTTAAAT	5149
QY	4158	CCTGGGGGATGGGTGGCGCCCAACTTGTCTCTCCAGCGCTGCTTCTGCTTTCTAGG	4217
Db	5150	CCTGGGGGATGGGTGGCGCCCAACTTGTCTCTCCAGCGCTGCTTCTGCTTTCTAGG	5209
QY	4218	CGCGGCAATCGTGAGCGGCTGTTGGCAGCATAGGCTTGGGAAGTGTCTGTGATAT	4277
Db	5210	CGCGGCAATCGTGAGCGGCTGTTGGCAGCATAGGCTTGGGAAGTGTCTGTGATAT	5269
QY	4278	TTTGGCAGGTTATGGAGCAGGGTGGCAGCGGCTCGTGGCCTTTAAGGTCATGAGCGG	4337
Db	5270	TTTGGCAGGTTATGGAGCAGGGTGGCAGCGGCTCGTGGCCTTTAAGGTCATGAGCGG	5329
QY	4338	CGAGATGCCCTCCACCGAGGACCTGGTTAACTACTCCCTGCTATCTCTCCCTGGCGC	4397
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QY	4398	CCTAGTCGTGGGTGCTGTCGAGCGCATCTGCTCGGCACTGGGCGGAGGAGG	4457
Db	5390	CCTAGTCGTGGGTGCTGTCGAGCGCATCTGCTCGGCACTGGGCGGAGGAGG	5449
QY	4458	GGCTGTGAGTGAATGAACCGGCTGATGCGTTGCTTCGGGGGTAAACAGTCTCCCC	4517
Db	5450	GGCTGTGAGTGAATGAACCGGCTGATGCGTTGCTTCGGGGGTAAACAGTCTCCCC	5509
QY	4518	CACGACTATGTGCTGAGAGCGAGTGTGAGCAGTGTACTCAGATCTCTCTAGTCT	4577
Db	5510	CACGACTATGTGCTGAGAGCGAGTGTGAGCAGTGTACTCAGATCTCTCTAGTCT	5569
QY	4578	TACCATCACTCAGTGTGAGAGGCTTCAACAGTGAATCAACAGGAGTGTCTCCAGGCC	4637
Db	5570	TACCATCACTCAGTGTGAGAGGCTTCAACAGTGAATCAACAGGAGTGTCTCCAGGCC	5629
QY	4638	ATGCTCGGCTCGTGGCTAGAGATGTTGGGATGATATGACGGTGTGACTGATTT	4697

Db	5630	ATGCTCGGCTCGTGGCTAAGAGATGTTGGGATTTGATATGACGGTGTGACTGATTT	5699
QY	4698	CAAGACTGTGCTCCAGTCCAAAGCTCTGCGCGCATTTGCCGGGAGTCCCTCTTCTCATG	4757
Db	5690	CAAGACTGTGCTCCAGTCCAAAGCTCTGCGCGCATTTGCCGGGAGTCCCTCTTCTCATG	5749
QY	4758	TCAACGTGGGTACAAAGGAGTCTGGGGGGGCGAGGCGATCATGCAAAACCACTGCCCATG	4817
Db	5750	TCAACGTGGGTACAAAGGAGTCTGGGGGGGCGAGGCGATCATGCAAAACCACTGCCCATG	5809
QY	4818	TGGAGCACAGATCACCGGACATGTGAAAACCGTTCCATGAGGATCGTGGGGCTAGGAC	4877
Db	5810	TGGAGCACAGATCACCGGACATGTGAAAACCGTTCCATGAGGATCGTGGGGCTAGGAC	5869
QY	4878	CTGTAGTAACAGTGTGCATGGAACATTCCTCCCATTAACGCGTACACACGGGCCCTGCAC	4937
Db	5870	CTGTAGTAACAGTGTGCATGGAACATTCCTCCCATTAACGCGTACACACGGGCCCTGCAC	5929
QY	4938	GCCCTCCCGGGCCAAATTTATTTCTAGGGGCTGTGGCGGCTGCTGAGGAGTACGT	4997
Db	5930	GCCCTCCCGGGCCAAATTTATTTCTAGGGGCTGTGGCGGCTGCTGAGGAGTACGT	5989
QY	4998	GGAGGTTACCGGGTGGGGATTTCCACTACGTGACGGGCGATGACCACTGACAACTGAA	5057
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QY	5058	GTGCGGCTGTCAGGTTCCGGCCCGGAAATTTCTCAAGAGTGGATGGGGTGGCTGCA	5117
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QY	5118	CAGGTACGCTCAGCGTGCACACCCCTCTCCTACGGGAGGAGTCACTTCTCGTGGGT	5177
Db	6110	CAGGTACGCTCAGCGTGCACACCCCTCTCCTACGGGAGGAGTCACTTCTCGTGGGT	6169
QY	5178	CAATCAATACCTGTTGGGTCAAGCTCCCATGCGAGCCCGAACCGGACGTAGCAGTGT	5237
Db	6170	CAATCAATACCTGTTGGGTCAAGCTCCCATGCGAGCCCGAACCGGACGTAGCAGTGT	6229
QY	5238	CACITTCATGCTCAGGACCCCTCCCAATTAAGCGGAGAGCGCTAAGCGTGGCTGGC	5297
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QY	5298	CAGGGGATCTCCCTCTGCGGCGCTCATCAGTACGAGCGCTGTCTGCGCTTCCTT	5357
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QY	5358	GAAAGCAATGCACTACCGTCACTGCTCCCGGACGCTGACCTCATCGAGGCCAACT	5417
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QY	5418	CCTGTGGCGGAGAGATGGCGGGAAATCAACCGCGTGGAGTCAGAAAAATAGGTAGT	5477
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QY	5478	AAATTTGCACTTTTCGAGCGCTCCAAAGCGGAGGAGATGAGAGGAGTATCGTTCC	5537
Db	6470	AAATTTGCACTTTTCGAGCGCTCCAAAGCGGAGGAGATGAGAGGAGTATCGTTCC	6529
QY	5538	GGCGGAGATCTGTGGAGGCTCCAGGAAATTCCTTCGAGCGATGCCATATGGGACCGCC	5597
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QY	5598	GGATTACAACTCTCAGTGTAGAGTCTTGAAGGACCCGAGTACGTCTCCAGTGGT	5657
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QY	5658	ACAGGCTGTCCATGCGGCTCCAGGCGCTCCGATACCACTCCAGGAGAGAG	5717
Db	6650	ACAGGCTGTCCATGCGGCTCCAGGCGCTCCGATACCACTCCAGGAGAGAG	6709
QY	5718	GACGGTGTCTGTCAAGATCTACCGTGTCTTCTGCTTGGCGAGTCCGCCAAGAC	5777
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QY	2178	CTTACTCTCCCGCAGGCGGCTCTCTACTTTGAAGGGCTCTTCGGGGCTCCACTGTCTCTG	2237	Db	4420	GTTTCGATTCCTCGGTTCTGTGGAGTGTCTATGACGGGGCTGTGCTGTGACGAGCTCAC	4479
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Db	3520	GGACAACTCGTCCCTCCGCGCTTACCGCAGACATTCACAGTGGCCCATCTACAGCCCC	3579	QY	3498	TACGGTGTGGCGCAGGGCTCAGGCTCCACCTCCATCGTGGGACCAAAATGTGGAGTGTCT	3557
QY	2418	TACTGTAGCGGCAAGACACTAAGGTGCCGGTGTGATGACGCCCAAGGGTATAGGT	2477	Db	4660	TACGGTGTGGCGCAGGGCTCAGGCTCCACCTCCATCGTGGGACCAAAATGTGGAGTGTCT	4719
Db	3580	TACTGTAGCGGCAAGACACTAAGGTGCCGGTGTGATGACGCCCAAGGGTATAGGT	3639	QY	3558	CATACCGCTAAAGCTACGCTGCA CGGGCCAAACGCCCCCTCTGTGTATAGGCTGGAGCGGT	3617
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Db	3760	CACGTACTCCACTATGCGCAAGTTTCTTGCCGACGGTGTGTCTCTGGGGCGGCTATGA	3819	QY	3738	CGGCTATTGGCTGACAA CAGGCGAGTGTGTCATTTGTGGGAGGATCATCTTTGTCCGAAA	3797
QY	2658	CATCATATATGATGAGTGCCACTCAACTGACTCGACCACTATCTGGGCATCGGCAC	2717	Db	4900	CGGCTATTGGCTGACAA CAGGCGAGTGTGTCATTTGTGGGAGGATCATCTTTGTCCGAAA	4959
Db	3820	CATCATATATGATGAGTGCCACTCAACTGACTCGACCACTATCTGGGCATCGGCAC	3879	QY	3798	GCGGGCCATCATTTCCGACAGGAGNAGTCTTTTACCGGGAGTTCATGATGAGAGAGTG	3857
QY	2718	AGTCTTGACCAAGCGAGAGCGGTGGAGCGGACTCGTGTGTCTCGCCACCGCTAGGCC	2777	Db	4960	GCGGGCCATCATTTCCGACAGGAGNAGTCTTTTACCGGGAGTTCATGATGAGAGAGTG	5019
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QY	2778	TCGGGATCGGTCAACCGTGCCATCCAAACATCGAGAGGTGTGTCTGACGACTGG	2837	Db	5020	CGCTCACACCTCCCTTACATCGAA CAGGGAATGACAGCTCGCCGAAACAAATTCACACAGAA	5079
Db	3940	TCGGGATCGGTCAACCGTGCCATCCAAACATCGAGAGGTGTGTCTGACGACTGG	3999	QY	3918	GGCAATCGGGTTGTGCAAA CAGCCACCAAGCAAGCGAGGCTGTCTCCCGTGTGGA	3977
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Db	4000	AGAAATCCCTTTTATGGCAAGGCATCCCATCGAGACCATCAAGGGGGGAGGCACCT	4059	QY	3978	ATCCAAAGTGGGAGCCCTCGAGAGTCTTGGCGAGCATATGTGGAATTTTCATCAGCGG	4037
QY	2898	CATTTCTGCCATTTCAAGAGAAATGTGATGAGCTCGCCGAGAGTGTCTCGGCTCGG	2957	Db	5140	ATCCAAAGTGGGAGCCCTCGAGAGTCTTGGCGAGCATATGTGGAATTTTCATCAGCGG	5199
Db	4060	CATTTCTGCCATTTCAAGAGAAATGTGATGAGCTCGCCGAGAGTGTCTCGGCTCGG	4119	QY	4038	GATACAAATTTTAGCAGGCTTGTCCACTCTGCTGGCAACCCCGCATAGCATCACTGAT	4097
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QY	3018	CGTCAATGCTAGCAACGAGCGCTTAATGACGGGCTTTACCGGCATTTTCGACTCAGT	3077	Db	5260	GGCAATTTCAAGCCTTATACCAAGCGGCTCCACCCCAACATACCTCTCTGTTTAAACAT	5319
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QY	3078	GATCGACTGCAATATGTGTACCCGACAGAGTTCAGCTTCAGCTTCGACCCGACCTTCAC	3137	Db	5320	CCTGGGGGATGGGTGGCGCCCAACTTGTCTCTCCAGCGCTGTCTCTGCTTTCTGATGG	5379
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Db	5440	TTTGGCAGGTTATGAGAGAGGGTGGCAGCGCGCTCGTGCCCTTTAAAGGTCATGAGCGG	5499
QY	4338	CGAGATCCCTCCACCCAGAGACCTGGTTAACTTACTCTCCCTGCTATCTCTCTCCCTGGCGC	4397
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Db	5560	CCTAGTCTGGGGTCTGTGTGCGCAGCGATACCTCGCTCGGACGCTGGGCCCCAGGGAGGG	5619
QY	4458	GGCTGTGACGTGGATGAACCGGCTGTATAGCGTTGCTTTCGCGGGTTAAACACGCTCTCCCC	4517
Db	5620	GGCTGTGACGTGGATGAACCGGCTGTATAGCGTTGCTTTCGCGGGTTAAACACGCTCTCCCC	5679
QY	4518	CACGCACTATGTGCTCGAGAGCGCTGACGACGCTGTCACTCAGATCCTCTCTAGTCT	4577
Db	5680	CACGCACTATGTGCTCGAGAGCGCTGACGACGCTGTCACTCAGATCCTCTCTAGTCT	5739
QY	4578	TACCATCACTCAGCTGCTGAAGAGGCTTCAACAGTGGATCAACGAGGACTGCTCCAGGCC	4637
Db	5740	TACCATCACTCAGCTGCTGAAGAGGCTTCAACAGTGGATCAACGAGGACTGCTCCAGGCC	5799
QY	4638	ATGCTCGGCTCGTGGCTAAGAGATTTGGGATTTGGATATGATCAACGCTGTGATGATTT	4697
Db	5800	ATGCTCGGCTCGTGGCTAAGAGATTTGGGATTTGGATATGATCAACGCTGTGATGATTT	5859
QY	4698	CAAGACTTGCTCCAGTCCAGGCTCTGCGCGATTTGGGAGTCCCGGAGTCCCTTCTCTCATG	4757
Db	5860	CAAGACTTGCTCCAGTCCAGGCTCTGCGCGATTTGGGAGTCCCGGAGTCCCTTCTCTCATG	5919
QY	4758	TCAACGTGGGTACAAAGGAGTCTGGGGGCGACGGCATCATGCAAAACACCTGCCCATG	4817
Db	5920	TCAACGTGGGTACAAAGGAGTCTGGGGGCGACGGCATCATGCAAAACACCTGCCCATG	5979
QY	4818	TGGAGACAGATCACCGGACATGTGAAAACCGTTCCATGAGGATCGTGGGGCTTAGGAC	4877
Db	5980	TGGAGACAGATCACCGGACATGTGAAAACCGTTCCATGAGGATCGTGGGGCTTAGGAC	6039
QY	4878	CTGTATTAACAGTGGCANTGGACATTTCCCATTAACGGGTACACACGGGCCCTTGAC	4937
Db	6040	CTGTATTAACAGTGGCANTGGACATTTCCCATTAACGGGTACACACGGGCCCTTGAC	6099
QY	4938	GCCCTCCCGGGCCAAATTTCTAGGGCGCTGTGGCGGGTGGCTGTGAGGAGTACGT	4997
Db	6100	GCCCTCCCGGGCCAAATTTCTAGGGCGCTGTGGCGGGTGGCTGTGAGGAGTACGT	6159
QY	4998	GGAGGTTAGCGGGTGGGGATTTCCAATACTGACGGGCATGACCACTGACAAAGTAA	5057
Db	6160	GGAGGTTAGCGGGTGGGGATTTCCAATACTGACGGGCATGACCACTGACAAAGTAA	6219
QY	5058	GTGCCGTGTGAGGTTCCGGCCCCCGAATTTCTCAAGAGTGGATGGGGTGGGTGCA	5117
Db	6220	GTGCCGTGTGAGGTTCCGGCCCCCGAATTTCTCAAGAGTGGATGGGGTGGGTGCA	6279
QY	5118	CAGGTACGCTCAGGTTCCGGCCCCCGAATTTCTCAAGAGTGGATGGGGTGGGTGCA	5177
Db	6280	CAGGTACGCTCAGGTTCCGGCCCCCGAATTTCTCAAGAGTGGATGGGGTGGGTGCA	6339
QY	5178	CAATCAATACCTGGTGGGTCAAGCTCCATTCGAGGAGGAGTCACTTCTGGTGGGCT	5237
Db	6340	CAATCAATACCTGGTGGGTCAAGCTCCATTCGAGGAGGAGTCACTTCTGGTGGGCT	6399
QY	5238	CACCTTCATGCTCACGACCCCTCCCATATACGGGGAGGAGCGGTAAAGCTAGGCTGGC	5297
Db	6400	CACCTTCATGCTCACGACCCCTCCCATATACGGGGAGGAGCGGTAAAGCTAGGCTGGC	6459
QY	5298	CAGGGGATCTCCCCCTCTCTGGCGAGCTCATCAGTACGAGCTGTCTGGCCCTTCTT	5357
Db	6460	CAGGGGATCTCCCCCTCTCTGGCGAGCTCATCAGTACGAGCTGTCTGGCCCTTCTT	6519
QY	5358	GAAGGCAACATGCACTACCGGTCACTGCTCCCGGACGCTGACCTCATCGAGGGCAACCT	5417

Db	6520	GAAGGCAACATGCACTACCGGTCACTGCTCCCGGACGCTGACCTCATCGAGGGCAACCT	6579
QY	5418	CTGTGGCGGAGAGATGGCGGGAAATCATCACCCGCTGGAGTCAAGAAATAGGTAGT	5477
Db	6580	CTGTGGCGGAGAGATGGCGGGAAATCATCACCCGCTGGAGTCAAGAAATAGGTAGT	6639
QY	5478	AATTTTGGACCTCTTTTCAGACCGCTCCAGCGGAGGAGATGAGAGGAAATATCCGTTCC	5537
Db	6640	AATTTTGGACCTCTTTTCAGACCGCTCCAGCGGAGGAGATGAGAGGAAATATCCGTTCC	6699
QY	5538	GGCGGAGATCCTTCGGAGGTCAGGAAATTCCTTCGAGCGATGCCCATATATGGCACGCC	5597
Db	6700	GGCGGAGATCCTTCGGAGGTCAGGAAATTCCTTCGAGCGATGCCCATATATGGCACGCC	6759
QY	5598	GGATTACAACCCCTCCACTGTTAGAGTCTCGAAAGGACCCCGGACTACGTCCTCCAGTGGT	5657
Db	6760	GGATTACAACCCCTCCACTGTTAGAGTCTCGAAAGGACCCCGGACTACGTCCTCCAGTGGT	6819
QY	5658	ACACGGGTGTCCTTCGCGGCTGCCAAGGCCCTCCGATACCACTCCACGGAGGAAGAG	5717
Db	6820	ACACGGGTGTCCTTCGCGGCTGCCAAGGCCCTCCGATACCACTCCACGGAGGAAGAG	6879
QY	5718	GACGGTGTCTCTCAGAAATCTACCGTGTCTCTGCTTGGCGGAGCTCGCCACAAGAC	5777
Db	6880	GACGGTGTCTCTCAGAAATCTACCGTGTCTCTGCTTGGCGGAGCTCGCCACAAGAC	6939
QY	5778	CTTCGGGACGCTCCGAAATCTGCGCCCTCGACAGCGGACGGCAACGGCCCTCTCTGACCA	5837
Db	6940	CTTCGGGACGCTCCGAAATCTGCGCCCTCGACAGCGGACGGCAACGGCCCTCTCTGACCA	6999
QY	5838	GCCCTCCGAGGAGCGGAGTCCGAGCGTGTGAGTCTCTCTCAATGCCCCCT	5897
Db	7000	GCCCTCCGAGGAGCGGAGTCCGAGCGTGTGAGTCTCTCTCAATGCCCCCT	7059
QY	5898	TGAGGGGAGCGGGGGATCCCGATCTCAGCGACGGGTCTTGGTCTACCGTAAAGCGAGA	5957
Db	7060	TGAGGGGAGCGGGGGATCCCGATCTCAGCGACGGGTCTTGGTCTACCGTAAAGCGAGA	7119
QY	5958	GGCTAGTAGGACGTGCTGCTGCTGATGCTCTACACATGAGGACAGGGCGCTGATCAC	6017
Db	7120	GGCTAGTAGGACGTGCTGCTGCTGATGCTCTACACATGAGGACAGGGCGCTGATCAC	7179
QY	6018	GCCATGCGTGGGAGGAAACCAAGTCCCATCAATGCACTGAGCAACTCTTTTGTCTCG	6077
Db	7180	GCCATGCGTGGGAGGAAACCAAGTCCCATCAATGCACTGAGCAACTCTTTTGTCTCG	7239
QY	6078	TCACCACAACTTGGTCTATGCTTACCAATCTCGCAGCGCAAGCTCGCGCAGGAAGCT	6137
Db	7240	TCACCACAACTTGGTCTATGCTTACCAATCTCGCAGCGCAAGCTCGCGCAGGAAGCT	7299
QY	6138	CACCTTTGACAGCTGCGAGGCTCTGACGACCACTACCGGGACGCTCTCAAGAGATGAA	6197
Db	7300	CACCTTTGACAGCTGCGAGGCTCTGACGACCACTACCGGGACGCTCTCAAGAGATGAA	7359
QY	6198	GGCGAAGGGTCCACAGTTAAGGCTAACTTCTATCCGTGGAGGAAGCTGTAAAGCTGAC	6257
Db	7360	GGCGAAGGGTCCACAGTTAAGGCTAACTTCTATCCGTGGAGGAAGCTGTAAAGCTGAC	7419
QY	6258	GCCCCCACAATTCGGCGAGATCTAAATTTGGCTATGGGGCAAGGACGTCGGGAACCTATC	6317
Db	7420	GCCCCCACAATTCGGCGAGATCTAAATTTGGCTATGGGGCAAGGACGTCGGGAACCTATC	7479
QY	6318	CAGCAAGCGCTTAAACCACTCCGCTCGTGTGGAGGACTTGTGGAGACACTTGAGAC	6377
Db	7480	CAGCAAGCGCTTAAACCACTCCGCTCGTGTGGAGGACTTGTGGAGACACTTGAGAC	7539
QY	6378	ACCAATTGACACCACTCATGCGAAATAATAGAGTTTCTGCGTCCAAACAGAGAAAGG	6437
Db	7540	ACCAATTGACACCACTCATGCGAAATAATAGAGTTTCTGCGTCCAAACAGAGAAAGG	7599
QY	6438	GGGCGGCAAGCGAGCTCGCTTATTCAGATTTGGGGGTTCTGCTGTGGGAA	6497

Db 7600 GGGCCGCAAGCAGCTCGCTTATTCATTCACAGATTGCGGGTTCGTGTGCGAGAA 7659  
Qy 6498 AATGGCCCTTTACATGTGTCTCCACCTCCCTCAGCGGTGATGGCTCTTCATACGG 6557  
Db 7660 AATGGCCCTTTACATGTGTCTCCACCTCCCTCAGCGGTGATGGCTCTTCATACGG 7719  
Qy 6558 ATTCCATATCTCTCCGACAGCGGTGAGTTCCTGTGTAATGCCCTGGAAGCGAAGAA 6617  
Db 7720 ATTCCATATCTCTCCGACAGCGGTGAGTTCCTGTGTAATGCCCTGGAAGCGAAGAA 7779  
Qy 6618 ATGCCCTATGGCTTCGATATGACACCCGCTGTTTGAACCTCAACGGTCACTGAGATGA 6677  
Db 7780 ATGCCCTATGGCTTCGATATGACACCCGCTGTTTGAACCTCAACGGTCACTGAGATGA 7839  
Qy 6678 CATCCGTGTGAGAGTCAATCTACCAATGTTGTGACTTGGCCGCCGGAAGCCACAGAGC 6737  
Db 7840 CATCCGTGTGAGAGTCAATCTACCAATGTTGTGACTTGGCCGCCGGAAGCCACAGAGC 7899  
Qy 6738 CATAGGTTCGCTCACAGAGCGCTTTACATCGGGGGCCCCCTGACTAATTTCTAAAGGSCA 6797  
Db 7900 CATAGGTTCGCTCACAGAGCGCTTTACATCGGGGGCCCCCTGACTAATTTCTAAAGGSCA 7959  
Qy 6798 GAACCTGGGCTATCGCCGGTCCCGGAGCGGTGTAAGACACCGAGCTCGGTTATAC 6857  
Db 7960 GAACCTGGGCTATCGCCGGTCCCGGAGCGGTGTAAGACACCGAGCTCGGTTATAC 8019  
Qy 6858 CCTCACATGTTACTGAAGGCGCTGCGGCTGTGAGCTGGAGCTCCAGGACTGCAC 6917  
Db 8020 CCTCACATGTTACTGAAGGCGCTGCGGCTGTGAGCTGGAGCTCCAGGACTGCAC 8079  
Qy 6918 GATGCTCGTATGCGGAGACGACTTGTGCTTATCTGTGAAGCGCGGGAACCAAGAGGA 6977  
Db 8080 GATGCTCGTATGCGGAGACGACTTGTGCTTATCTGTGAAGCGCGGGAACCAAGAGGA 8139  
Qy 6978 CGAGCGAGCTACGGGCTTTACGAGGCTATGACTAGATACCTGCCCCCTCGGGGA 7037  
Db 8140 CGAGCGAGCTACGGGCTTTACGAGGCTATGACTAGATACCTGCCCCCTCGGGGA 8199  
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Db 8200 CCGGCCCAACAGATACGACTTGGAGTTGATACATCATGCTCTCCATGTGTCACT 8259  
Qy 7098 CGCGCAGCATGATCTGCAAAAGGCTGTACTATCTCACCGGTGACCCACACCCCTCT 7157  
Db 8260 CGCGCAGCATGATCTGCAAAAGGCTGTACTATCTCACCGGTGACCCACACCCCTCT 8319  
Qy 7158 TGCGCGGCTCGTGGGAGACAGCTAGACACACTCCAGTCAATTCCTGGCTAGGCAACAT 7217  
Db 8320 TGCGCGGCTCGTGGGAGACAGCTAGACACACTCCAGTCAATTCCTGGCTAGGCAACAT 8379  
Qy 7218 CATCATGTATGGCCACACTTGTGGGCAAGGATGATCCTGATGACTCATTTCTTCCAT 7277  
Db 8380 CATCATGTATGGCCACACTTGTGGGCAAGGATGATCCTGATGACTCATTTCTTCCAT 8439  
Qy 7278 CTTCTAGCTCAGGAACACTTGAAGAAAGCCCTAGATTCTCAGATCTACGGGCTGTGA 7337  
Db 8440 CTTCTAGCTCAGGAACACTTGAAGAAAGCCCTAGATTCTCAGATCTACGGGCTGTGA 8499  
Qy 7338 CTTCCATTGAGCCACTTGAACCTACCTCAGATCATTTCAACGACTCCATGGCTTAGGCAAT 7397  
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Qy 7398 TTCACTCCATAGTACTCTCCAGGTGAGATCAATAGGTTGGCTTCAATGCTCAGGAACCT 7457  
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Qy 7458 TGGGGTACCGCCCTTGGGAGTCTGGAGACATCGGGCCAGAAAGTGTCCGGCTAGGCTACT 7517  
Db 8620 TGGGGTACCGCCCTTGGGAGTCTGGAGACATCGGGCCAGAAAGTGTCCGGCTAGGCTACT 8679  
Qy 7518 GTCCCAAGGGGGAGGGCTGCGACCTTGTGGCAAGTACCTTCTCAACTGGGCAGTAAGGAC 7577  
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Qy 7578 CAAGCTCAAACTCACTCCAAATCCCGGCTGCGTCCCAAGTTGGAATTTATCCAGCTGCTCGT 7637  
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Qy 7638 TGCTGGTTACAGCGGGGAGACATATATACAGCTGTCTCGTCCCGACCCCGCTCGTT 7697  
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Qy 7698 CATGTGTGCTACTCTCTACTTTCTGTAGGGTAGGCATCTATCTACTCCCCAACCGATG 7757  
Db 8860 CATGTGTGCTACTCTCTACTTTCTGTAGGGTAGGCATCTATCTACTCCCCAACCGATG 8919  
Qy 7758 AACGGGAGCTAAACACTCCAGGCAATAGGCCAATCTGTTTTTTTCCCTTTTTTTTTT 7817  
Db 8920 AACGGGAGCTAAACACTCCAGGCAATAGGCCAATCTGTTTTTTTCCCTTTTTTTTTT 8979  
Qy 7818 CTTT 7877  
Db 8980 CTTT 9039  
Qy 7878 CTTTTTTTCTTTTGGTGGTCCCATCTTAGCCCTTAGTCACGGCTAGCTGTGAAAGTCCG 7937  
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Search completed: November 9, 2004, 06:45:56  
Job time : 21434 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 19:28:28 ; Search time 2220 Seconds  
(without alignments)  
18897.916 Million cell updates/sec

Title: US-10-005-469-1

Perfect score: 7992

Sequence: 1 gccagcccccagattggggggc.....ctctctgcagatcaagact 7992

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: geneseqn1990s.\*  
3: geneseqn2000s.\*  
4: geneseqn2001as.\*  
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10: geneseqn2003cs.\*  
11: geneseqn2003ds.\*  
12: geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7992	100.0	7992	6	AAL47276 Hepatitis
2	7992	100.0	10690	6	ABK91412 Hepatitis
3	7992	100.0	10690	9	ACA61697 Hepatitis
4	7992	100.0	10690	10	ADC83762 Hepatitis
5	7990.4	100.0	7992	6	AAL47281 Hepatitis
6	7990.4	100.0	10690	6	ABK91448 Hepatitis
7	7990.4	100.0	10690	6	ABK91435 Hepatitis
8	7990.4	100.0	10690	6	ABK91243 Hepatitis
9	7990.4	100.0	10690	6	ABK91434 Hepatitis
10	7990.4	100.0	11313	12	ADP86264 Hepatitis
11	7989	100.0	7989	3	AAA98968 Hepatitis
12	7989	100.0	7989	12	ADJ57845 HCV repli
13	7988.8	100.0	10690	6	ABK91440 Hepatitis
14	7988.8	100.0	11313	12	ADP86271 Hepatitis
15	7987.4	99.9	7989	6	AAD25322 Hepatitis
16	7987.2	99.9	7992	6	AAL47280 Hepatitis
17	7987.2	99.9	7992	6	AAL47277 Hepatitis
18	7987.2	99.9	11313	12	ADP86265 Hepatitis
19	7985.8	99.9	7989	6	AAD25326 Hepatitis
20	7985.6	99.9	11313	12	ADP86272 Hepatitis
21	7984	99.9	10690	6	ABK91242 Hepatitis

22	7982.6	99.9	7989	6	AAD25325 Hepatitis
23	7982.6	99.9	7989	10	ADD93734 Hepatitis
24	7982.4	99.9	11313	12	ADP86275 Hepatitis
25	7981	99.9	10691	6	ABK91423 Hepatitis
26	7980.8	99.9	11313	12	ADP86273 Hepatitis
27	7979.2	99.8	11313	12	ADP86266 Hepatitis
28	7979	99.8	10693	6	ABK91438 Hepatitis
29	7977.6	99.8	11313	12	ADP86268 Hepatitis
30	7977.4	99.8	10693	6	ABK91443 Hepatitis
31	7976.2	99.8	10691	6	ABK91439 Hepatitis
32	7975	99.8	7987	6	AAD25321 Hepatitis
33	7974.4	99.8	11313	12	ADP86267 Hepatitis
34	7973.6	99.8	7991	6	AAL47279 Hepatitis
35	7973.4	99.8	7987	6	AAD25329 Hepatitis
36	7971.8	99.7	7987	6	AAD25324 Hepatitis
37	7967	99.7	8001	3	AAA98967 Hepatitis
38	7966.2	99.7	7995	6	AAL47278 Hepatitis
39	7958.4	99.6	11313	12	ADP86270 Hepatitis
40	7955.2	99.5	11313	12	ADP86269 Hepatitis
41	7777.8	97.3	7989	10	ADD93733 Hepatitis
42	7714.4	96.5	11184	12	ADP86274 Hepatitis
43	7706.4	96.4	11184	12	ADP86276 Hepatitis
44	7701.6	96.4	11184	12	ADP86277 Hepatitis
45	7695.4	96.3	7848	6	AAD25323 Hepatitis

## ALIGNMENTS

RESULT 1  
AAL47276  
ID AAL47276 standard; DNA; 7992 BP.  
XX  
AC AAL47276;  
XX  
DT 30-AUG-2002 (first entry)  
XX  
DE Hepatitis C virus sub-genomic replicon clone 1377-NS3-3'UTR.

XX Hepatitis; HCV; core-neo; NS3 proteinase/helicase; vaccine; diagnosis;  
XX virucide; hepatotropic; gene therapy; anti-viral; gene; ds.

XX Hepatitis C virus.

Key	Location/Qualifiers
CDS	342..1181
FT	/*tag= a
FT	/product= "core-neo fusion protein"
FT	1801..7758
FT	/*tag= b
FT	/product= "NS3 proteinase/helicase"

XX WO200238793-A2.

XX 16-MAY-2002.

XX 02-NOV-2001; 2001WO-US046350.

XX 07-NOV-2000; 2000US-0245866P.

XX (ANAD-) ANADYS PHARM INC.

XX Bichke V;

XX WPI; 2002-490082/52.

XX P-PSDB; AA018000, AA018001.

XX Novel nucleic acid encoding replication competent recombinant hepatitis C virus genome useful for screening anti-hepatitis C virus therapeutics and for vaccine development.

XX Claim 6; Page 43-47; 85pp; English.

CC The present invention provides protein and coding sequences from  
CC Hepatitis C virus (HCV), comprising all or part of the HCV genome and  
CC able to replicate efficiently when transfected into a susceptible cell  
CC line without reducing the growth rate of the cell line by more than 10  
CC fold. The sequences are useful for screening for anti-HCV therapeutics,  
CC for detecting antibodies to HCV in a biological sample such as blood,  
CC serum, plasma, blood cells, lymphocytes, or liver cells from a subject,  
CC for deriving authentic HCV components such as replication-complement non-  
CC infectious, replication-defective infection-component, and replication-  
CC defective non-infectious HCV, in gene therapy or gene vaccination  
CC targeted to hepatic tissue for treating an animal infected or susceptible  
CC to HCV infection and for studying HCV infection and propagation. The  
CC present sequence is a clone of a fragment of the HCV genome which encodes  
CC the core-neo and NS3 proteinase/helicase proteins  
XX

SQ Sequence 7992 BP; 1648 A; 2369 C; 2243 G; 1732 T; 0 U; 0 Other;

Query Match		100.0%;	Score 7992;	DB 6;	Length 7992;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 7992;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GCCAGCCCCCGATTGGGGGCGACATCCACATAGATCACTCCCTCTGTGAGGAATCTACTG	60		
DB	1	GCCAGCCCCCGATTGGGGGCGACATCCACATAGATCACTCCCTCTGTGAGGAATCTACTG	60		
QY	61	TCTTACGACGAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTGCGAGCCCTCCAGGAC	120		
DB	61	TCTTACGACGAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTGCGAGCCCTCCAGGAC	120		
QY	121	CCCCCTCCCGGAGAGCCATAGTGTCTCGGAAACGGGTGAGTACACCGGAATTCGCCAG	180		
DB	121	CCCCCTCCCGGAGAGCCATAGTGTCTCGGAAACGGGTGAGTACACCGGAATTCGCCAG	180		
QY	181	GACGACCGGGTCCCTTTCTTGGATCAACCCCGCTCAATGCCCTGAGAGATTGGGGCGTGC	240		
DB	181	GACGACCGGGTCCCTTTCTTGGATCAACCCCGCTCAATGCCCTGAGAGATTGGGGCGTGC	240		
QY	241	GCAGACTGTAGCGAGTAGTGTGGTTCGGAAGAGCCCTGTGTACTGCTGATAGG	300		
DB	241	GCAGACTGTAGCGAGTAGTGTGGTTCGGAAGAGCCCTGTGTACTGCTGATAGG	300		
QY	301	GTGCTTCGAGTGTGCGGAGGCTCTGTAGACCGTGCACCATGAGCACGAATCTTAAC	360		
DB	301	GTGCTTCGAGTGTGCGGAGGCTCTGTAGACCGTGCACCATGAGCACGAATCTTAAC	360		
QY	361	CTCAAGAAACCAAAAGGCGCGCCATGATTTGAACAAGATGGATTGCACGAGGTTCTC	420		
DB	361	CTCAAGAAACCAAAAGGCGCGCCATGATTTGAACAAGATGGATTGCACGAGGTTCTC	420		
QY	421	CGGCGGCTTGGGTGAGAGGCTATTTCGGCTATGACTGGCACACACACATCGGCTGCT	480		
DB	421	CGGCGGCTTGGGTGAGAGGCTATTTCGGCTATGACTGGCACACACACATCGGCTGCT	480		
QY	481	CTGATGCGCGCTGTTCGGCTGTACGCGAGGGGCGCCGGTTCTTTTGTCAAGACCG	540		
DB	481	CTGATGCGCGCTGTTCGGCTGTACGCGAGGGGCGCCGGTTCTTTTGTCAAGACCG	540		
QY	541	ACCTGTCCGFGCCCTGAATGAACCTGACGAGCGAGCGCGCGCTATCGTGGCTGGCCA	600		
DB	541	ACCTGTCCGFGCCCTGAATGAACCTGACGAGCGAGCGCGCGCTATCGTGGCTGGCCA	600		
QY	601	CGAGCGGCTTCTTGGCGAGCTGTCTGACGTTGTTCATGAAAGCGGGAAGGACTGGC	660		
DB	601	CGAGCGGCTTCTTGGCGAGCTGTCTGACGTTGTTCATGAAAGCGGGAAGGACTGGC	660		
QY	661	TGCTATTGGGGAAGTCCGGGCGAGGATCTCTGTATCTCACTTGTCTCTGCGGAGA	720		
DB	661	TGCTATTGGGGAAGTCCGGGCGAGGATCTCTGTATCTCACTTGTCTCTGCGGAGA	720		
QY	721	AAGTATCCATCATGCTGTATGAATGCGGCGGCTGCATACGTTGATCCGCTACTGCC	780		
DB	721	AAGTATCCATCATGCTGTATGAATGCGGCGGCTGCATACGTTGATCCGCTACTGCC	780		

QY	781	CATTGACCAACAAGCGGAAAATCCGATCGAGCGAGCAGTACTCGGATGGAAGCGGTC	840		
DB	781	CATTGACCAACAAGCGGAAAATCCGATCGAGCGAGCAGTACTCGGATGGAAGCGGTC	840		
QY	841	TTGTGATCAGGATGATCTGACGAGAGAGCATCAGGGCTCGCGCCAGCCGAACTGTCG	900		
DB	841	TTGTGATCAGGATGATCTGACGAGAGAGCATCAGGGCTCGCGCCAGCCGAACTGTCG	900		
QY	901	CCAGGCTCAAGGCGCGCATGCCCAGCGGAGATCTCGTGTGACCCATGCGATGCTT	960		
DB	901	CCAGGCTCAAGGCGCGCATGCCCAGCGGAGATCTCGTGTGACCCATGCGATGCTT	960		
QY	961	GCTTCCCGAATATCATGTGTGAAAATGCGCGCTTTTCTGGATTCATCGACTGCGCGG	1020		
DB	961	GCTTCCCGAATATCATGTGTGAAAATGCGCGCTTTTCTGGATTCATCGACTGCGCGG	1020		
QY	1021	TGGGTGTGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTTGATATGCTGAAGAGC	1080		
DB	1021	TGGGTGTGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTTGATATGCTGAAGAGC	1080		
QY	1081	TTGGGGCGGAATGGGCTGACCGCTTCTCGTGTGTTTACCGGTATCGCGCTCCCGATTCG	1140		
DB	1081	TTGGGGCGGAATGGGCTGACCGCTTCTCGTGTGTTTACCGGTATCGCGCTCCCGATTCG	1140		
QY	1141	AGCGATTCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCAACAG	1200		
DB	1141	AGCGATTCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCAACAG	1200		
QY	1201	GTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTAACCTTACTGGC	1260		
DB	1201	GTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTAACCTTACTGGC	1260		
QY	1261	CGAAGCGCTTGAATAAGCGCGTGTGCGTTTGTCTATATGTTATTTTCCACATATG	1320		
DB	1261	CGAAGCGCTTGAATAAGCGCGTGTGCGTTTGTCTATATGTTATTTTCCACATATG	1320		
QY	1321	CGCTCTTTTGGCAATGTGAGGCGCGGAAACCTTGGGCTGTCTTCTTGAAGAGATTCCT	1380		
DB	1321	CGCTCTTTTGGCAATGTGAGGCGCGGAAACCTTGGGCTGTCTTCTTGAAGAGATTCCT	1380		
QY	1381	AGGGCTCTTTCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCA	1440		
DB	1381	AGGGCTCTTTCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCA	1440		
QY	1441	GTTCCTCTGGAAGCTTCTTGAAGCAAAACGTCGTAGCGACCTTTTCAGCGACGG	1500		
DB	1441	GTTCCTCTGGAAGCTTCTTGAAGCAAAACGTCGTAGCGACCTTTTCAGCGACGG	1500		
QY	1501	AACCCCTCTGCGACAGTGTGCTGCGCCAAAGCCACGTGTATAGATACACCT	1560		
DB	1501	AACCCCTCTGCGACAGTGTGCTGCGCCAAAGCCACGTGTATAGATACACCT	1560		
QY	1561	GCAAGCGGCAACAACCCAGTGCACGTTGTGAGTTGGATGTTGTGGAAGAGTCAAA	1620		
DB	1561	GCAAGCGGCAACAACCCAGTGCACGTTGTGAGTTGGATGTTGTGGAAGAGTCAAA	1620		
QY	1621	TGGCTCTCTCAAGCGTATTCAACAAGGCTGAAGGATGCCAGAGGTACCCATTTGT	1680		
DB	1621	TGGCTCTCTCAAGCGTATTCAACAAGGCTGAAGGATGCCAGAGGTACCCATTTGT	1680		
QY	1681	ATGGGATCTGATCTGGGGCTCTCGTGCACATGTTTACATGTTTGTAGTCGAGGTTAAA	1740		
DB	1681	ATGGGATCTGATCTGGGGCTCTCGTGCACATGTTTACATGTTTGTAGTCGAGGTTAAA	1740		
QY	1741	AACCTCTAGGCGCCCGCAACACCGGGGACGTGGTTTCTTTGAAAACACAGATATACC	1800		
DB	1741	AACCTCTAGGCGCCCGCAACACCGGGGACGTGGTTTCTTTGAAAACACAGATATACC	1800		
QY	1801	ATGGCGCTATTAGCGCTACTCCCAACAGACGCGGACCTTACTTGGCTGATCATCACT	1860		
DB	1801	ATGGCGCTATTAGCGCTACTCCCAACAGACGCGGACCTTACTTGGCTGATCATCACT	1860		
QY	1861	AGCTTCACAGGCGCGGACAGGAACCGAGTTCGAGGGGAGGTCCAAAGTGTCTCCACCGCA	1920		

1861 AGCTCTACAGCGCGGACAGGAAACCAAGGTCCAGGGAGGTCCAAGTGGTCTCCACGCA 1920  
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Db 3481 CTGCTAGCATACGAGGCTACGCTGTGCGCAGGCTCAGGCTCCACCTTCGTTGGGAC 3540  
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QY	4141	ACCCTCCTGTTTAAACATCTGGGGGGATGGGGTGGCCGCCAACTTGTCTCTCCAGCGCT	4200	QY	5221	CGGACGTAGCAGTGTCTCATTCCATGTCTACCGACCCCTCCCAATTTACCGCGAGACG	5280
Db	4141	ACCCTCCTGTTTAAACATCTGGGGGGATGGGGTGGCCGCCAACTTGTCTCTCCAGCGCT	4200	Db	5221	CGGACGTAGCAGTGTCTCATTCCATGTCTACCGACCCCTCCCAATTTACCGCGAGACG	5280
QY	4201	GCTTCTGCTTTCTAGGCGCCGCGCATTCGTGAGCGGCTGTGGCAGCATAGGCCCTTGGG	4260	QY	5281	GCTAAGCGTAGGCTGGCCAGGGGATCTCCGCCCTCTTGGCCAGCTCATCAGCTAGCCAG	5340
Db	4201	GCTTCTGCTTTCTAGGCGCCGCGCATTCGTGAGCGGCTGTGGCAGCATAGGCCCTTGGG	4260	Db	5281	GCTAAGCGTAGGCTGGCCAGGGGATCTCCGCCCTCTTGGCCAGCTCATCAGCTAGCCAG	5340
QY	4261	AGGTGCTTGTGATATTTTGGCAGTTATGAGCAGGGGTGGCAGCGCGCTCGTGGCC	4320	QY	5341	CTGTCTGGCCTTCTTGAAGCAACATGCACTACCCGTCATGATCTCCCGAGCGTAC	5400
Db	4261	AGGTGCTTGTGATATTTTGGCAGTTATGAGCAGGGGTGGCAGCGCGCTCGTGGCC	4320	Db	5341	CTGTCTGGCCTTCTTGAAGCAACATGCACTACCCGTCATGATCTCCCGAGCGTAC	5400
QY	4321	TTTAAAGGTCAAGCGCGGAGATGCCCTCCACCGAGGACCTGGTTAACTACTCCCTGCT	4380	QY	5401	CTCATCGAGCCAACTCTCTGTGGGGCAGAGATGGGCGGAAATCATCACCCGCTGGAG	5460
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QY	4381	ATCCTCTCCCTGGCGCCCTAGTGTGCGGGTCTGTGGCAGCGATCTGCGTGGCAC	4440	QY	5461	TCAGAAATTAAGGTAGTAAATTTTGGACTCTTTTCGAGCCGCTCCAGCGGAGGAGTAC	5520
Db	4381	ATCCTCTCCCTGGCGCCCTAGTGTGCGGGTCTGTGGCAGCGATCTGCGTGGCAC	4440	Db	5461	TCAGAAATTAAGGTAGTAAATTTTGGACTCTTTTCGAGCCGCTCCAGCGGAGGAGTAC	5520
QY	4441	GTGGGCCAGGGAGGGGCTGTGAGTGAACCGGCTGATAGGTTGCTTCCGCTCGCG	4500	QY	5521	AGGAAAGTATCGTTCGGGGGAGATCTCGCGAGGTCCAGGAAATTTCCCTCGAGCGATG	5580
Db	4441	GTGGGCCAGGGAGGGGCTGTGAGTGAACCGGCTGATAGGTTGCTTCCGCTCGCG	4500	Db	5521	AGGAAAGTATCGTTCGGGGGAGATCTCGCGAGGTCCAGGAAATTTCCCTCGAGCGATG	5580
QY	4501	GGTAAACAGTCTCCCGCCAGCACTATGTGCTGAGAGCGACGTGCGACAGTGTCACT	4560	QY	5581	CCCATATGGGCAAGCGCGGATTAACACCTTCCACTGTTAGAGTCTTGGAAAGACCCGGAC	5640
Db	4501	GGTAAACAGTCTCCCGCCAGCACTATGTGCTGAGAGCGACGTGCGACAGTGTCACT	4560	Db	5581	CCCATATGGGCAAGCGCGGATTAACACCTTCCACTGTTAGAGTCTTGGAAAGACCCGGAC	5640
QY	4561	CAGATCCTCTAGTCTTACCATCATCTCAGTGTGTAAGAGGCTTCCAGAGTGGATCAAC	4620	QY	5641	TACGTCCTCCAGTGTATACAGGCTTCCATTCGCGCTCCAGAGGCCCTCCGATACCA	5700
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QY	4681	ACGCTGTGACTGATTTCAAGACCTGGCTCCAGTCCAGGCTCTGCGCGGATTCGCGGA	4740	QY	5761	GAGCTGCCACAAAGACCTTTCGGCAGCTCCGAAATCTGTCGCGCTCGACAGCGCACGCA	5820
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QY	4741	GTCCCTTCTTCAATGTAAGTGGGTACAGGAGTCTGGCGGGGCGAGCGATCATG	4800	QY	5821	ACGCGCTCTCTGACAGCGCTTCGACGAGCGCGGATCCGATCTCAGCGACGGGTCTTGG	5940
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QY	4861	ATCGTGGGCTTAGGACTGTAGTAAACAGTGGATGAAATTCCTCCCATTAACGCTAC	4920	QY	6001	ACAGCGCTGTATACGCGCATGCGCTGCGGAGGAAACCAAGCTGCCATCAATGCACTG	6060
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QY	4921	ACCAAGGCGCTGACGCGCTTCCCGCGGCGCAATTTATCTAGGCGCTGTGGGGGTG	4980	QY	6061	AGCAACTTTTCTCGCTCCGTCACCAACCTTGTCTATGTCTATGTAACATCTTCGAGCGCAAGC	6120
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QY	5041	ACCACTGACAAAGTAAAGTGGCGGTGAGTGTGAGTTCGGGCGCGCAATTTCTTACAGAGTG	5100	QY	6121	CTGGGCGGAGAGAGGTACCTTTGACAGATGTCAGGTCTTGGAGCGACCATCCCGGAGC	6180
Db	5041	ACCACTGACAAAGTAAAGTGGCGGTGAGTGTGAGTTCGGGCGCGCAATTTCTTACAGAGTG	5100	Db	6121	CTGGGCGGAGAGAGGTACCTTTGACAGATGTCAGGTCTTGGAGCGACCATCCCGGAGC	6180
QY	5101	GATGGGTGCGTTCACAGATGATCGCTCCAGCGTGCACACCCCTCTCAGGAGGAGGTC	5160	QY	6181	GTGCTCAAGGAGATGAAGCGGAGGCGCTCCAGTTTAAAGCTTAACTTCTATCCGTTGAG	6240
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FT /label= IRES
FT /note= "Internal ribosome entry site from EMCV"
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FT /tag= f
FT /note= "Plasmid derived sequences"
XX WO200259321-A2.
XX 01-AUG-2002.
XX 16-JAN-2002; 2002WO-BP000526.
XX 23-JAN-2001; 2001US-0263479P.
XX (RICE-) IST RICERCHIE BIOL MOLECOLARE ANGELETTI.
XX De Francesco R, Migliaccio G, Paonessa G;
XX WPI; 2002-599793/84.
XX New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
XX NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
XX ribosome entry site (IRES) region, useful in studying HCV replication and
XX expression.
XX Claim 1; Fig 1; 69pp; English.
XX The invention relates to nucleic acid molecules comprising altered HCV
XX NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
XX internal ribosome entry site (IRES) region coding for one or more NS3,
XX NS5A, or EMCV IRES mutations, respectively. The location of the mutations
XX are detailed in the specification. Also included are (1) an expression
XX vector comprising a nucleotide sequence coding for the altered nucleic
XX acids, which is transcriptionally coupled to an exogenous promoter; (2) a
XX recombinant cell human hepatoma cell comprising the altered nucleic acids
XX; (3) a recombinant cell produced by introducing into a human hepatoma
XX cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
XX replicon enhanced cell or which containing a functional HCV replicon; (5)
XX an HCV replicon enhanced cells made in the method; and (6) measuring the
XX ability of a compound to affect HCV activity. The HCV replicons and HCV
XX replicon enhanced cells are useful in studying HCV replication and
XX expression, and HCV and host cell interactions, producing HCV RNA and
XX proteins, and providing a system for measuring the ability of a compound
XX to modulate one or more HCV activities e.g. to discover drugs which may
XX treat HCV mediated diseases such as liver failure, cirrhosis and
XX hepatocellular carcinoma. The present sequence is the HCV based vector
XX pHCVNeo.17, used as a basis for the adaptive mutations of the invention
XX
XX Sequence 10690 BP; 2334 A; 3045 C; 2908 G; 2403 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 7992; DB 6; Length 10690;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 7992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 721 AAGTATCCATCATGCTGATGCAATGCGGCGGTGATGCTGCTGATGCTGCTGCTGCTG 780
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QY	1381	AGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAAATGTCTGAAGGAAGCA	1440
Db	1381	AGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAAATGTCTGAAGGAAGCA	1440
QY	1441	GTTCTCTGGAAGCTTCTTTGAAGCAAAACAAGCTCTGTAGGAGCCCTTTGCAAGCAGCGG	1500
Db	1441	GTTCTCTGGAAGCTTCTTTGAAGCAAAACAAGCTCTGTAGGAGCCCTTTGCAAGCAGCGG	1500
QY	1501	AACCCGCCACCTGGCGACAGGTGCTCTCGGCCAAAGCCACAGCTGTATTAAGATACACCT	1560
Db	1501	AACCCGCCACCTGGCGACAGGTGCTCTCGGCCAAAGCCACAGCTGTATTAAGATACACCT	1560
QY	1561	GCAAGGGCGCACAAACCCAGTGCACGTTGTGAGTTGGATAGTTGTGAAAGAGTCAAA	1620
Db	1561	GCAAGGGCGCACAAACCCAGTGCACGTTGTGAGTTGGATAGTTGTGAAAGAGTCAAA	1620
QY	1621	TGGCTCTCCTCAAGGTAATTCAAACAAGGGCTGAAGATGCCAGAGGTACCCCATTTGT	1680
Db	1621	TGGCTCTCCTCAAGGTAATTCAAACAAGGGCTGAAGATGCCAGAGGTACCCCATTTGT	1680
QY	1681	ATGGGATCTGATCTGGGGCTTCGGTGACATGCTTTTACATGTTTGTAGTTCGAGGTTAAAA	1740
Db	1681	ATGGGATCTGATCTGGGGCTTCGGTGACATGCTTTTACATGTTTGTAGTTCGAGGTTAAAA	1740
QY	1741	AAGCTTAGGCCCCCGGAAACACCGGGGACGTGGTTTCCCTTTGAAAGAACAGATAATACC	1800
Db	1741	AAGCTTAGGCCCCCGGAAACACCGGGGACGTGGTTTCCCTTTGAAAGAACAGATAATACC	1800
QY	1801	ATGGCGCTATTAGGCTCTACTTCCAAACAGCGGAGGCTACTTGGCTGCATCATCACT	1860
Db	1801	ATGGCGCTATTAGGCTCTACTTCCAAACAGCGGAGGCTACTTGGCTGCATCATCACT	1860
QY	1861	AGGCTCACAGCCGGGACAGAACCCAGCTCGAGGGGAGGTCCAAAGTGGTCTCCACCGCA	1920
Db	1861	AGGCTCACAGCCGGGACAGAACCCAGCTCGAGGGGAGGTCCAAAGTGGTCTCCACCGCA	1920
QY	1921	ACAAATCTTCTGGCGACTGGTCAATGGGCTGTGTTGGACTGTCTATCATGTGGCC	1980
Db	1921	ACAAATCTTCTGGCGACTGGTCAATGGGCTGTGTTGGACTGTCTATCATGTGGCC	1980
QY	1981	GGCTCAAGACCTTGGCCGCCAAAGGGCCCAATCACCCAAATGTACACCAATGTGGAC	2040
Db	1981	GGCTCAAGACCTTGGCCGCCAAAGGGCCCAATCACCCAAATGTACACCAATGTGGAC	2040
QY	2041	CAGGACTCTGTCGGCTGGCAAGCGCCCGCGGGCGGTTCTTGTACACCATGCACTGC	2100
Db	2041	CAGGACTCTGTCGGCTGGCAAGCGCCCGCGGGCGGTTCTTGTACACCATGCACTGC	2100
QY	2101	GGGAGCTCGGACTTTACTTGGTTCAGAGGCAATGCCGATGTCATTCGGGTGCGCCGCGG	2160
Db	2101	GGGAGCTCGGACTTTACTTGGTTCAGAGGCAATGCCGATGTCATTCGGGTGCGCCGCGG	2160
QY	2161	GGGAGCAGCAGGGGAGGCTACTCTCCCGCAGCCCGTCTCTTATGAAAGGCTCTTCG	2220
Db	2161	GGGAGCAGCAGGGGAGGCTACTCTCCCGCAGCCCGTCTCTTATGAAAGGCTCTTCG	2220
QY	2221	GGCGGTCCACTGCTCTGCCCTCGGGGCAAGCTGTGGGATCTTTTGGGCTGCCGTGTGC	2280
Db	2221	GGCGGTCCACTGCTCTGCCCTCGGGGCAAGCTGTGGGATCTTTTGGGCTGCCGTGTGC	2280
QY	2281	ACCCGAGGGGTTCGGAAGGGGTGACTTTTGTACCCGTGAGTCTATGGAACCACTATG	2340
Db	2281	ACCCGAGGGGTTCGGAAGGGGTGACTTTTGTACCCGTGAGTCTATGGAACCACTATG	2340
QY	2341	CGGTCCCGGTCTTTCAGGCAAACTCGTCCCTCGGCCGTACCGGAGACATTTCCAGGTG	2400
Db	2341	CGGTCCCGGTCTTTCAGGCAAACTCGTCCCTCGGCCGTACCGGAGACATTTCCAGGTG	2400
QY	2401	GCCCATCTACAGCCCTTACTTGGTAGCGGCAAGAGCACTAAGGTGCGGCTATGCA	2460
Db	2401	GCCCATCTACAGCCCTTACTTGGTAGCGGCAAGAGCACTAAGGTGCGGCTATGCA	2460
QY	2461	GCCCAAGGTTAAGGTGCTTGTCTGAAACCGCTCGCTCGCCGACCCCTAGGTTTCGGG	2520
Db	2461	GCCCAAGGTTAAGGTGCTTGTCTGAAACCGCTCGCTCGCCGACCCCTAGGTTTCGGG	2520
QY	2521	CGGTATATGTCTAAGGACATGCTATCGACCTTAACATCAGAACCGGGGTAGGACCATC	2580
Db	2521	CGGTATATGTCTAAGGACATGCTATCGACCTTAACATCAGAACCGGGGTAGGACCATC	2580
QY	2581	ACCAAGGTTGCCCCCATCACTACTCCACCTATGGAAGTTTCTTGGCCGAGGTTGTC	2640
Db	2581	ACCAAGGTTGCCCCCATCACTACTCCACCTATGGAAGTTTCTTGGCCGAGGTTGTC	2640
QY	2641	TCTGGGGCGCTATGACATCATTAATATGTGATGAGTGCCACTCACTGACTCGACCAT	2700
Db	2641	TCTGGGGCGCTATGACATCATTAATATGTGATGAGTGCCACTCACTGACTCGACCAT	2700
QY	2701	ATCTTGGGCTATCGGACAGTCTCTGGAACCAAGCGGAGACGGCTGGAGCGGACTCGTGTG	2760
Db	2701	ATCTTGGGCTATCGGACAGTCTCTGGAACCAAGCGGAGACGGCTGGAGCGGACTCGTGTG	2760
QY	2761	CTGCCACCGTACGCTCTCGGGATCGGTCAACCGTGCACATCCAAACATCGAGGAGTG	2820
Db	2761	CTGCCACCGTACGCTCTCGGGATCGGTCAACCGTGCACATCCAAACATCGAGGAGTG	2820
QY	2821	GCTCTGCCAGCACTGGAGAAATCCCTTTTATGGCAAGGCAATCCCATCGAGACCATC	2880
Db	2821	GCTCTGCCAGCACTGGAGAAATCCCTTTTATGGCAAGGCAATCCCATCGAGACCATC	2880
QY	2881	AAGGGGGGAGGACCTCTATTTCTGCAATTCGAAGAAATGTGATGAGTCTCGCGCG	2940
Db	2881	AAGGGGGGAGGACCTCTATTTCTGCAATTCGAAGAAATGTGATGAGTCTCGCGCG	2940
QY	2941	AAGGTGTCGGCTCTGAGTCAATGTGTAGCATATTAACGGGCGCTTGTATGTCGCTC	3000
Db	2941	AAGGTGTCGGCTCTGAGTCAATGTGTAGCATATTAACGGGCGCTTGTATGTCGCTC	3000
QY	3001	ATACCAACTAGCGGAGACCTCATTTCTGTAGCAACCGACGCTCTAATGACGGCTTTACC	3060
Db	3001	ATACCAACTAGCGGAGACCTCATTTCTGTAGCAACCGACGCTCTAATGACGGCTTTACC	3060
QY	3061	GGCGATTTTCGACTCACTGATCGACTGCAATATCATGTGTCAACCCAGACAGTCTCAGC	3120
Db	3061	GGCGATTTTCGACTCACTGATCGACTGCAATATCATGTGTCAACCCAGACAGTCTCAGC	3120
QY	3121	CTGGACCGGACCTTCACTTGAAGACGACCGTGCACAGACGGGTGTCAACGCTCG	3180
Db	3121	CTGGACCGGACCTTCACTTGAAGACGACCGTGCACAGACGGGTGTCAACGCTCG	3180
QY	3181	CAGCGCGAGGAGGAGGCTGTAGGGGACAGTGGGCAATTTACAGTTTGTGACTCCAGGA	3240
Db	3181	CAGCGCGAGGAGGAGGCTGTAGGGGACAGTGGGCAATTTACAGTTTGTGACTCCAGGA	3240
QY	3241	GAAAGGCGCTCGGGGCAATGTTCCGATTTCTGTGAGTGTCTATGACGGGGCTGT	3300
Db	3241	GAAAGGCGCTCGGGGCAATGTTCCGATTTCTGTGAGTGTCTATGACGGGGCTGT	3300
QY	3301	GCTTGTGACAGTCAAGCTCAAGCTTCAAGTGTGAGGCTTACCTTAAACACA	3360
Db	3301	GCTTGTGACAGTCAAGCTCAAGCTTCAAGTGTGAGGCTTACCTTAAACACA	3360
QY	3361	CCAGGGTTGCCGTCTGCCAGGACCATCTGAGATTTCTGGGAGAGCGTCTTTACGGCTTC	3420
Db	3361	CCAGGGTTGCCGTCTGCCAGGACCATCTGAGATTTCTGGGAGAGCGTCTTTACGGCTTC	3420
QY	3421	ACCCACATAGAGCCCATTTCTTGTCCAGACTTAAGCAGGAGGAGACACTTCCCTTAC	3480
Db	3421	ACCCACATAGAGCCCATTTCTTGTCCAGACTTAAGCAGGAGGAGACACTTCCCTTAC	3480

Db	3421	ACCCACATAGACGCCCATTTCTTCTCCAGACTAAGCAGGCGAGAGCAACTTCCCTAC	3480	Qy	4561	CAGATCCTCTCTAGTCTTACCATCACTCAGCTGTGAAGAGGCTTACCAGTGGATCAAC	4620
Qy	3481	CTGTAGCATACAGGCTACGGTGTGCGCCAGGGCTCAGGCTCCACCTCCATCTGGGAC	3540	Db	4561	CAGATCCTCTCTAGTCTTACCATCACTCAGCTGTGAAGAGGCTTACCAGTGGATCAAC	4620
Db	3481	CTGTAGCATACAGGCTACGGTGTGCGCCAGGGCTCAGGCTCCACCTCCATCTGGGAC	3540	Qy	4621	GAGGACTGTCTCAGCCATGCTCCGGCTCGGTCTAAGAGATGTTTGGATTGGATATGC	4680
Qy	3541	CAAAATGTGGAAGTGTCTCATACGGCTAAAGCTACGCTGCAGCGGCCCAACGCCCTCTGTG	3600	Db	4621	GAGGACTGTCTCAGCCATGCTCCGGCTCGGTCTAAGAGATGTTTGGATTGGATATGC	4680
Db	3541	CAAAATGTGGAAGTGTCTCATACGGCTAAAGCTACGCTGCAGCGGCCCAACGCCCTCTGTG	3600	Qy	4681	ACGGTGTGAGTCTTCAATGTCGCTCAAGGAGTCTCGGCGGGGCGACCGGATCATG	4740
Qy	3601	TATAGGCTGGGAGCGGCTTCAAAACAGAGTTACTACCAACACCCCATAAACCAATATATC	3660	Db	4681	ACGGTGTGAGTCTTCAATGTCGCTCAAGGAGTCTCGGCGGGGCGACCGGATCATG	4740
Db	3601	TATAGGCTGGGAGCGGCTTCAAAACAGAGTTACTACCAACACCCCATAAACCAATATATC	3660	Qy	4741	GTCCCTCTTCTTCTCATGTCGCTCAAGGAGTCTCGGCGGGGCGACCGGATCATG	4800
Qy	3661	ATGGCATGATGTGCGCTGACCTGAGGTGCTCAGGACCTGAGTGTGTTAGGCGGA	3720	Db	4741	GTCCCTCTTCTTCTCATGTCGCTCAAGGAGTCTCGGCGGGGCGACCGGATCATG	4800
Db	3661	ATGGCATGATGTGCGCTGACCTGAGGTGCTCAGGACCTGAGTGTGTTAGGCGGA	3720	Qy	4801	CAAAACACCTGCGGCTTGGAGCAGATCACCGGACATGTGAAACCGTTCATATGAGG	4860
Qy	3721	GTCCCTAGCAGCTCTGGCGCGTATTGCTGACAAACAGGCGAGCTGCTCATTTGTGGGAGG	3780	Db	4801	CAAAACACCTGCGGCTTGGAGCAGATCACCGGACATGTGAAACCGTTCATATGAGG	4860
Db	3721	GTCCCTAGCAGCTCTGGCGCGTATTGCTGACAAACAGGCGAGCTGCTCATTTGTGGGAGG	3780	Qy	4861	ATCGTGGGCGCTTAGGACCTGTAGTAAACAGTGGCATGGAACATTCCTCCATTAACCGTAC	4920
Qy	3781	ATCATCTTTGTCGGAAAGCGGCCATCATTTCCGACAGGGAAGTCTTTTACGGGAGTTTC	3840	Db	4861	ATCGTGGGCGCTTAGGACCTGTAGTAAACAGTGGCATGGAACATTCCTCCATTAACCGTAC	4920
Db	3781	ATCATCTTTGTCGGAAAGCGGCCATCATTTCCCGACAGGGAAGTCTTTTACGGGAGTTTC	3840	Qy	4921	ACCACGGGCGCTTGACCGCTCTCCCGCGCCCAAAATTATTCTAGGGCGCTGTGGCGGTTG	4980
Qy	3841	GATGAGTGAAGTGGCGCTCACACCTCCCTTACATCGACAGGAGTGCAGCTCGCC	3900	Db	4921	ACCACGGGCGCTTGACCGCTCTCCCGCGCCCAAAATTATTCTAGGGCGCTGTGGCGGTTG	4980
Db	3841	GATGAGTGAAGTGGCGCTCACACCTCCCTTACATCGACAGGGAATGCAGCTCGCC	3900	Qy	4981	GCTGTGAGGAGTACGTGGAGTTACCGGGTGGGGGATTTCCACTACGTGACGGGCATG	5040
Qy	3901	GAACAATTCACACAGAGGCAATCGGTTGCTGCAAAACAGCCACCAAGCAAGCGGAGGCT	3960	Db	4981	GCTGTGAGGAGTACGTGGAGTTACCGGGTGGGGGATTTCCACTACGTGACGGGCATG	5040
Db	3901	GAACAATTCACACAGAGGCAATCGGTTGCTGCAAAACAGCCACCAAGCAAGCGGAGGCT	3960	Qy	5041	ACCACCTGACCAAGTAAAGTGGCGCTCAGGTTCCGGGCGCCCGAAATTTCTTACAGAGTG	5100
Qy	3961	GCTGCTCCGCTGGTGAATTCAGTGGCGGACCTCTGAAAGCCCTTTGGCGGAGCATATG	4020	Db	5041	ACCACCTGACCAAGTAAAGTGGCGCTCAGGTTCCGGGCGCCCGAAATTTCTTACAGAGTG	5100
Db	3961	GCTGCTCCGCTGGTGAATTCAGTGGCGGACCTCTGAAAGCCCTTTGGCGGAGCATATG	4020	Qy	5101	GATGGGTGCGGTGTCACAGGTACGCTCCAGGTGCAAAACCCCTCTCTACGGGAGGAGTTC	5160
Qy	4021	TGGAATTCATCAGCGGATACAAATTTAGCAGGCTTTCCACTCTGCTGCGCAACCCC	4080	Db	5101	GATGGGTGCGGTGTCACAGGTACGCTCCAGGTGCAAAACCCCTCTCTACGGGAGGAGTTC	5160
Db	4021	TGGAATTCATCAGCGGATACAAATTTAGCAGGCTTTCCACTCTGCTGCGCAACCCC	4080	Qy	5161	ACATTCCTGCTGGGTCAATCAATACCTGTTGGTTCACAGTCCCATCGGAGCCGAA	5220
Qy	4081	GGATAGCATCACTGATGCAATTCACAGCTCTATCACCAGCCCGCTCACCACCCCAACAT	4140	Db	5161	ACATTCCTGCTGGGTCAATCAATACCTGTTGGTTCACAGTCCCATCGGAGCCGAA	5220
Db	4081	GGATAGCATCACTGATGCAATTCACAGCTCTATCACCAGCCCGCTCACCACCCCAACAT	4140	Qy	5221	CCGAGCTAGCAGTCTCATTCCATGCTCACCGACCCCTCCACATTAACGGCGGAGACG	5280
Qy	4141	ACCCTCCTGTTAAATCTTGGGGGATGCGTGGCGGCCCAACTGCTCTCCAGCGCT	4200	Db	5221	CCGAGCTAGCAGTCTCATTCCATGCTCACCGACCCCTCCACATTAACGGCGGAGACG	5280
Db	4141	ACCCTCCTGTTAAATCTTGGGGGATGCGTGGCGGCCCAACTGCTCTCCAGCGCT	4200	Qy	5281	GCTAAGCTAGGCTGGCCAGGGGATCTCCCTCTCTTGGCCAGCTCATCAGTAGCCAG	5340
Qy	4201	GCTTCTGCTTCTAGCGCGGCATCGCTGGAGCGGCTGTGGCAGCATAGGCTTGGG	4260	Db	5281	GCTAAGCTAGGCTGGCCAGGGGATCTCCCTCTCTTGGCCAGCTCATCAGTAGCCAG	5340
Db	4201	GCTTCTGCTTCTAGCGCGGCATCGCTGGAGCGGCTGTGGCAGCATAGGCTTGGG	4260	Qy	5341	CTGTCTGCGCTTCTTGAAGGCAACATGACCTACCCGTCATGACTCCCGGACGCTGAC	5400
Qy	4261	AAGGTGCTGTGATATTTGGCAGGTTATGGAGCAGGGGTGGCAGCGCGCTCGTGCC	4320	Db	5341	CTGTCTGCGCTTCTTGAAGGCAACATGACCTACCCGTCATGACTCCCGGACGCTGAC	5400
Db	4261	AAGGTGCTGTGATATTTGGCAGGTTATGGAGCAGGGGTGGCAGCGCGCTCGTGCC	4320	Qy	5401	CTCATCGAGGCCAACCTCTCTGTGGCGGAGAGATGGCGGGAAATCAACCCGCTGGAG	5460
Qy	4321	TTTAAAGTCATGAGCGCGAGATGCGCTCACCAGAGACCTGGTTAACTTACCTGCT	4380	Db	5401	CTCATCGAGGCCAACCTCTCTGTGGCGGAGAGATGGCGGGAAATCAACCCGCTGGAG	5460
Db	4321	TTTAAAGTCATGAGCGCGAGATGCGCTCACCAGAGACCTGGTTAACTTACCTGCT	4380	Qy	5461	TCAGAAAAATAGGTAGTAAATTTTGGACTCTTTTCGAGCCGCTCCAAAGCGGAGGATGAG	5520
Qy	4381	ATCCTCTCCCTGCGCGCTTGTCTGCGGCTGCTGCGCAGCATGCTGCGGCAC	4440	Db	5461	TCAGAAAAATAGGTAGTAAATTTTGGACTCTTTTCGAGCCGCTCCAAAGCGGAGGATGAG	5520
Db	4381	ATCCTCTCCCTGCGCGCTTGTCTGCGGCTGCTGCGCAGCATGCTGCGGCAC	4440	Qy	5521	AGGGAAGTATCCGTTCCGCGGAGATCCTCGGAGGTCCAGGAAATTTCCCTCGAGCGATG	5580
Qy	4441	GTGGGCCAGGGAGGGGCTGTGCACTGGATGAACCGGCTGATAGCGTTGCTTCCGG	4500	Db	5521	AGGGAAGTATCCGTTCCGCGGAGATCCTCGGAGGTCCAGGAAATTTCCCTCGAGCGATG	5580
Db	4441	GTGGGCCAGGGAGGGGCTGTGCACTGGATGAACCGGCTGATAGCGTTGCTTCCGG	4500	Qy	5581	CCCATATGGGACCGCCCGGATTAACCCCTCCACTGTTAGAGTCTCTGGAAGGACCCGAC	5640
Qy	4501	GGTAACCAACGCTCTCCCCCAGCACTATGTGCTGAGAGCGAGCGCTGAGCAAGTCACT	4560	Db	5581	CCCATATGGGACCGCCCGGATTAACCCCTCCACTGTTAGAGTCTCTGGAAGGACCCGAC	5640
Db	4501	GGTAACCAACGCTCTCCCCCAGCACTATGTGCTGAGAGCGAGCGCTGAGCAAGTCACT	4560				

QY	5641	TACGTCCTCCAGTGGTACAGCGGTGTCATTTGCCGCTGCGAAGGCCCTCCGATACCA	5700	Db	6721	CCCGAAGCCAGACAGCCATAAGGTCGCTCAGAGCGGCTTTTACATCGGGGGCCCCCTTG	6780
Db	5641	TACGTCCTCCAGTGGTACAGCGGTGTCATTTGCCGCTGCGAAGGCCCTCCGATACCA	5700	QY	6781	ACTAATTTCTAAGGCGAAGACTGCGGCTATCGCGGTGCGCGGCGAGCGGTGTACTGACG	6840
QY	5701	CCTCCACGAGGAGGAGCGGTGTCCTGTGTCAGAACTTACCGTGTCTCTGCTTGGG	5760	Db	6781	ACTAATTTCTAAGGCGAAGACTGCGGCTATCGCGGTGCGCGGCGAGCGGTGTACTGACG	6840
Db	5701	CCTCCACGAGGAGGAGCGGTGTCCTGTGTCAGAACTTACCGTGTCTCTGCTTGGG	5760	QY	6841	ACCGCTCGGGTAAATACCCCTCACATGTTACTTGAAGGCGGCTGCGGCTGTGAGCTGCG	6900
QY	5761	GAGCTCGCCACAAAGACCTTCGGCAGCTCCGAATCGTGGCGGTGCGACAGCGGCACGCCA	5820	Db	6841	ACCGCTCGGGTAAATACCCCTCACATGTTACTTGAAGGCGGCTGCGGCTGTGAGCTGCG	6900
Db	5761	GAGCTCGCCACAAAGACCTTCGGCAGCTCCGAATCGTGGCGGTGCGACAGCGGCACGCCA	5820	QY	6901	AAGCTCCAGGACTGCGCATGCTCGATGCGGAGACGACCTTGTCTGTATCTGTGAAAGC	6960
QY	5821	ACGGCTCTCTGACACGCCCTTCGACAGCGCGGAGCGCGGATCCGAGTTCGAGTTCGTAC	5880	Db	6901	AAGCTCCAGGACTGCGCATGCTCGATGCGGAGACGACCTTGTCTGTATCTGTGAAAGC	6960
Db	5821	ACGGCTCTCTGACACGCCCTTCGACAGCGCGGAGCGCGGATCCGAGTTCGAGTTCGTAC	5880	QY	6961	GCGGGACCCAAAGAGGACGAGCGGAGCTACGGGCTTCAAGGAGCTATGACTAGATAC	7020
QY	5881	TCCTCCATGCCCCCTTGAAGGGGAGCGGGGATCCGATCTCAGCGAGCGGCTTTGG	5940	Db	6961	GCGGGACCCAAAGAGGACGAGCGGAGCTACGGGCTTCAAGGAGCTATGACTAGATAC	7020
Db	5881	TCCTCCATGCCCCCTTGAAGGGGAGCGGGGATCCGATCTCAGCGAGCGGCTTTGG	5940	QY	7021	TCTGCCCCCTCGGGACCCGCCAAACCAAGTACGACTTGGAGTTGATACATCATGTC	7080
QY	5941	TCTACCGTAAAGGAGGCTAGTGAGGACGTCGTCGCTGCTCGATGCTTACACATGG	6000	Db	7021	TCTGCCCCCTCGGGACCCGCCAAACCAAGTACGACTTGGAGTTGATACATCATGTC	7080
Db	5941	TCTACCGTAAAGGAGGCTAGTGAGGACGTCGTCGCTGCTCGATGCTTACACATGG	6000	QY	7081	TCCTCCATGTCAGTCGCGCACGATGTCATCTGSCAAAAGGGTGTACTATCTCACCCGT	7140
QY	6001	ACAGCGCCCTGATCACGCCATGCGCTCGGAGGAAACCAAGCTGCCCATCAATGCACTG	6060	Db	7081	TCCTCCATGTCAGTCGCGCACGATGTCATCTGSCAAAAGGGTGTACTATCTCACCCGT	7140
Db	6001	ACAGCGCCCTGATCACGCCATGCGCTCGGAGGAAACCAAGCTGCCCATCAATGCACTG	6060	QY	7141	GACCCCAACCCCTTGGCGCGGCTGCGGGAGACAGCTAGACACACTCCAGTCAAT	7200
QY	6061	AGCAACTCTTTGCTCCGTCACCAACTTGTGTCATGTCATAAATCTCGAGCGCAAGC	6120	Db	7141	GACCCCAACCCCTTGGCGCGGCTGCGGGAGACAGCTAGACACACTCCAGTCAAT	7200
Db	6061	AGCAACTCTTTGCTCCGTCACCAACTTGTGTCATGTCATAAATCTCGAGCGCAAGC	6120	QY	7201	TCCTGGCTAGGACACATCATGATGCGGCCACCTTGTGGGCAAGATGATCCTGATG	7260
QY	6121	CTGCGGAGAAAGGTCACCTTTGACAGACTGCGAGTCTCTGGAGCAACACTACCGGAC	6180	Db	7201	TCCTGGCTAGGACACATCATGATGCGGCCACCTTGTGGGCAAGATGATCCTGATG	7260
Db	6121	CTGCGGAGAAAGGTCACCTTTGACAGACTGCGAGTCTCTGGAGCAACACTACCGGAC	6180	QY	7261	ACTCATTTCTTCCATCTTCTAGCTCAGGAAACACTTCAAAAAGCCCTAGATTGTTCAG	7320
QY	6181	GTGCTCAGGAGATCAAGGCGAAGCGCTCAGCTTAAAGCTTAACTTCTATCCGTGAG	6240	Db	7261	ACTCATTTCTTCCATCTTCTAGCTCAGGAAACACTTCAAAAAGCCCTAGATTGTTCAG	7320
Db	6181	GTGCTCAGGAGATCAAGGCGAAGCGCTCAGCTTAAAGCTTAACTTCTATCCGTGAG	6240	QY	7321	ATCTACGGGGCTGTACTCCATGACCACTTGACCTACCTCAGATCAITCAACGACTC	7380
QY	6241	GAAGCTGTAACTGACGCGCCCACTTCCGCGAGATCTAAATTTGGCTATGGGCAAG	6300	Db	7321	ATCTACGGGGCTGTACTCCATGACCACTTGACCTACCTCAGATCAITCAACGACTC	7380
Db	6241	GAAGCTGTAACTGACGCGCCCACTTCCGCGAGATCTAAATTTGGCTATGGGCAAG	6300	QY	7381	CATGGCCTTAGGCATTTTCACTCCATAGTATCTCTCAGGTGAGATCAATAGGGTGGCT	7440
QY	6301	GAGCTCGGAACCTTATCCAGCAAGCGGTTAAACCACTCCGCTCCGTGTGGAAGGACTTG	6360	Db	7381	CATGGCCTTAGGCATTTTCACTCCATAGTATCTCTCAGGTGAGATCAATAGGGTGGCT	7440
Db	6301	GAGCTCGGAACCTTATCCAGCAAGCGGTTAAACCACTCCGCTCCGTGTGGAAGGACTTG	6360	QY	7441	TCATGCTCAGGAAACTTGGGGTACCGCCCTTGGAGTCTGGAGTCTGGAGACATCGGGCCAGAGT	7500
QY	6361	CTGGAAGACTGAGACACCAATTTGACCAACATCATGCGAATAAATGAGGTTTCTGC	6420	Db	7441	TCATGCTCAGGAAACTTGGGGTACCGCCCTTGGAGTCTGGAGTCTGGAGACATCGGGCCAGAGT	7500
Db	6361	CTGGAAGACTGAGACACCAATTTGACCAACATCATGCGAATAAATGAGGTTTCTGC	6420	QY	7501	GTCCGCGCTAGGCTACTGTCCCAGGGGGAGGGCTGCCACTTTGTGGCAAGTACCTCTTC	7560
QY	6421	GTCCAAACGAGAGGGGGCGGCAAGCGAGCTCGCTTATCGTATTCAGATTGGGG	6480	Db	7501	GTCCGCGCTAGGCTACTGTCCCAGGGGGAGGGCTGCCACTTTGTGGCAAGTACCTCTTC	7560
Db	6421	GTCCAAACGAGAGGGGGCGGCAAGCGAGCTCGCTTATCGTATTCAGATTGGGG	6480	QY	7561	AACCTGGGCTAGGAGGAGGCTCAAACTCACTCCATCCCGCTGCGTCCCGAGTTGGAT	7620
QY	6481	GTTCTGTGTGCGAGAAATGGCCCTTACGATGTGGTCTCCACCTCCCTCAGGCGGTG	6540	Db	7561	AACCTGGGCTAGGAGGAGGCTCAAACTCACTCCATCCCGCTGCGTCCCGAGTTGGAT	7620
Db	6481	GTTCTGTGTGCGAGAAATGGCCCTTACGATGTGGTCTCCACCTCCCTCAGGCGGTG	6540	QY	7621	TTATCCAGCTGGTTCGTTGCTGTGTTACAGGGGGGAGACATATATCACGCCCTGTCTCGT	7680
QY	6541	ATGGGCTCTTCAACGATTCGATCTCTCTGGAGCGGGTTCGATGAGTTCCTGGTGAAT	6600	Db	7621	TTATCCAGCTGGTTCGTTGCTGTGTTACAGGGGGGAGACATATATCACGCCCTGTCTCGT	7680
Db	6541	ATGGGCTCTTCAACGATTCGATCTCTCTGGAGCGGGTTCGATGAGTTCCTGGTGAAT	6600	QY	7681	GCCCGACCCCGCTGTTGTTGCTGCTTCTTACTTCTTCTAGGGGTAGGCATCTAT	7740
QY	6601	GCTTGAAGAGGAGAAATGCGCTTATGGGCTTCGATATGACACCCGCTGTTTGAATCA	6660	Db	7681	GCCCGACCCCGCTGTTGTTGCTGCTTCTTACTTCTTCTAGGGGTAGGCATCTAT	7740
Db	6601	GCTTGAAGAGGAGAAATGCGCTTATGGGCTTCGATATGACACCCGCTGTTTGAATCA	6660	QY	7741	CTACTCCCCCAACCGATGAGGAGGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTT	7800
QY	6661	ACGGTCACTGAGAAATGACATCCGCTGTTGAGGAGTCAATCTACCAATGTTGTGACTTGGCC	6720	Db	7741	CTACTCCCCCAACCGATGAGGAGGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTT	7800
Db	6661	ACGGTCACTGAGAAATGACATCCGCTGTTGAGGAGTCAATCTACCAATGTTGTGACTTGGCC	6720	QY	7801	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
QY	6721	CCCGAAGCCAGACAGGCCATAGGTCGCTCAGAGCGGCTTTTACATCGGGGGCCCCCTTG	6780				



Db 661 TGCTATTGGCGAAGTGC CGGGCAGAGATCTCTGTCACTCACTTGTCTCTGCCGAGA 720  
QY 721 AAGTATCCATCATGGCTGATGCAATCGCGGCTGCATACGCTTGTGATCGGCTACCTGCC 780  
Db 721 AAGTATCCATCATGGCTGATGCAATCGCGGCTGCATACGCTTGTGATCGGCTACCTGCC 780  
QY 781 CATTCGACCAACAGGAAACATCGCATCGAGGAGCAGCTACTCGGATGGAAGCCGGTC 840  
Db 781 CATTCGACCAACAGGAAACATCGCATCGAGGAGCAGCTACTCGGATGGAAGCCGGTC 840  
QY 841 TTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGACCTGTTGG 900  
Db 841 TTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGACCTGTTGG 900  
QY 901 CAGGCTCAAGGGCGCATGCCCGACGCGGAGGATCTCGTGTGACCCATGCGCATGCCCT 960  
Db 901 CAGGCTCAAGGGCGCATGCCCGACGCGGAGGATCTCGTGTGACCCATGCGCATGCCCT 960  
QY 961 GCTTGCAGAAATCATGGTGGAAATGCGCGCTTTTCTGGATTCATCGACTGTGCGCGGC 1020  
Db 961 GCTTGCAGAAATCATGGTGGAAATGCGCGCTTTTCTGGATTCATCGACTGTGCGCGGC 1020  
QY 1021 TGGTGTGCGGACCGCTATCAGGACATAGCGTTGGCTACCGTGATATTGCTGAGAGC 1080  
Db 1021 TGGTGTGCGGACCGCTATCAGGACATAGCGTTGGCTACCGTGATATTGCTGAGAGC 1080  
QY 1081 TTGGCGGGAATGCGCTTCCTCGTCTTTACGGTATCGCGCTCCCGATTGCG 1140  
Db 1081 TTGGCGGGAATGCGCTTCCTCGTCTTTACGGTATCGCGCTCCCGATTGCG 1140  
QY 1141 AGCGATCGCTTCATCGCTTCTTGAAGAGTCTTCTGAGTTTAAACAGACCAACG 1200  
Db 1141 AGCGATCGCTTCATCGCTTCTTGAAGAGTCTTCTGAGTTTAAACAGACCAACG 1200  
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCTTACGGTATCGCGCTCCCGATTGCG 1260  
Db 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCTTACGGTATCGCGCTCCCGATTGCG 1260  
QY 1261 CGAAGCCGCTTGAATAAGCGGCTGCGTTTGTCTATATGTTATTTTCCACCATATTG 1320  
Db 1261 CGAAGCCGCTTGAATAAGCGGCTGCGTTTGTCTATATGTTATTTTCCACCATATTG 1320  
QY 1321 CCGTCTTTTGAATAGCGGCGCGGAAACCTGCGCTCTCTCTTGAAGAGCATTCCT 1380  
Db 1321 CCGTCTTTTGAATAGCGGCGCGGAAACCTGCGCTCTCTCTTGAAGAGCATTCCT 1380  
QY 1381 AGGGTCTTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGCTGCAAGGAGCA 1440  
Db 1381 AGGGTCTTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGCTGCAAGGAGCA 1440  
QY 1441 GTTTCCTCTGAAGCTTCTTGAAGCAAAACACGTCTGTAGCGACCTTTTGCAGCAGCGG 1500  
Db 1441 GTTTCCTCTGAAGCTTCTTGAAGCAAAACACGTCTGTAGCGACCTTTTGCAGCAGCGG 1500  
QY 1501 AACCCCGCTCTGCGACAGTCTCTGCGGCCAAGCCACGTGTATAGATACACCT 1560  
Db 1501 AACCCCGCTCTGCGACAGTCTCTGCGGCCAAGCCACGTGTATAGATACACCT 1560  
QY 1561 GCAAGGCGGCAACACCCAGTGCACGTGTGAGTTGGATGAGTTGGAAAGAGTCAAA 1620  
Db 1561 GCAAGGCGGCAACACCCAGTGCACGTGTGAGTTGGATGAGTTGGAAAGAGTCAAA 1620  
QY 1621 TGGCTCTCTCAAGCTATTCAACAGGGGTGAAGGATGCCAAGAGGTACCCCATTTG 1680  
Db 1621 TGGCTCTCTCAAGCTATTCAACAGGGGTGAAGGATGCCAAGAGGTACCCCATTTG 1680  
QY 1681 ATGGATCTCATCTGGGGCTCTGTCACATGCTTTTACATGTTTGTAGTTCGAGTTAAA 1740  
Db 1681 ATGGATCTCATCTGGGGCTCTGTCACATGCTTTTACATGTTTGTAGTTCGAGTTAAA 1740  
QY 1741 AAGCTCTAGGCCCCCGGAAACACGCGGACGTGTTTCTTTGAAACACGATATACC 1800  
Db 1741 AAGCTCTAGGCCCCCGGAAACACGCGGACGTGTTTCTTTGAAACACGATATACC 1800

QY 1801 ATGGCGCTATTACGCGCTACTCCCAACAGACGCGAGGCGCTACTTGGCTGCATCATCACT 1860  
Db 1801 ATGGCGCTATTACGCGCTACTCCCAACAGACGCGAGGCGCTACTTGGCTGCATCATCACT 1860  
QY 1861 AGCCTCACAGGCGCGGACAGAGAACAGGTTCGAGGGGAGGTCCAAAGTGTCTCCACCGCA 1920  
Db 1861 AGCCTCACAGGCGCGGACAGAGAACAGGTTCGAGGGGAGGTCCAAAGTGTCTCCACCGCA 1920  
QY 1921 ACACATCTTTCTGCGACCTTCGCTCAATGCGGTGTGTGGACTGTCTATCATGTGTC 1980  
Db 1921 ACACATCTTTCTGCGACCTTCGCTCAATGCGGTGTGTGGACTGTCTATCATGTGTC 1980  
QY 1981 GGTCTCAAGACCTTTGCGCGCCCAAGGCCCCCAATCACCACCAATGTGAC 2040  
Db 1981 GGTCTCAAGACCTTTGCGCGCCCAAGGCCCCCAATCACCACCAATGTGAC 2040  
QY 2041 CAGGACCTCGTCTGCGCTGCAAGCGCCCCCGGGCGCGTTCTTGACACCATGCACTGC 2100  
Db 2041 CAGGACCTCGTCTGCGCTGCAAGCGCCCCCGGGCGCGTTCTTGACACCATGCACTGC 2100  
QY 2101 GGCAGCTCGGACCTTTACTTGTGTCAGAGGCAATGCGATGTCTATTCGCGTGC CGCGG 2160  
Db 2101 GGCAGCTCGGACCTTTACTTGTGTCAGAGGCAATGCGATGTCTATTCGCGTGC CGCGG 2160  
QY 2161 GGCAGCAGCAGGGGAGCCTACTCTCCCGCAGGCGCGTCTCTTCTGAGGGCTCTTTCG 2220  
Db 2161 GGCAGCAGCAGGGGAGCCTACTCTCTCCCGCAGGCGCGTCTCTTCTGAGGGCTCTTTCG 2220  
QY 2221 GCGGTCTCACTGCTCTGCGCTCGGGCAGCGCTGTGGGCACTTTTCGGGCTCGCGTGTGC 2280  
Db 2221 GCGGTCTCACTGCTCTGCGCTCGGGCAGCGCTGTGGGCACTTTTCGGGCTCGCGTGTGC 2280  
QY 2281 ACCGAGGGTTCGAAAGCGGTGGAATTTGTACCCGTCGAGTCTATGAAACCACTATG 2340  
Db 2281 ACCGAGGGTTCGAAAGCGGTGGAATTTGTACCCGTCGAGTCTATGAAACCACTATG 2340  
QY 2341 CGGTCCCGGCTTTCACGCAAACTCGTCCCTCGGCGCTGACGAGACATTCAGGTG 2400  
Db 2341 CGGTCCCGGCTTTCACGCAAACTCGTCCCTCGGCGCTGACGAGACATTCAGGTG 2400  
QY 2401 GCCCATCTACAGCGCTTACTGTGTAGCGGCAAGAGACTAAGGTGCGGCTGCGTATGCA 2460  
Db 2401 GCCCATCTACAGCGCTTACTGTGTAGCGGCAAGAGACTAAGGTGCGGCTGCGTATGCA 2460  
QY 2461 GCCCAAGGTATAGGTGCTTGTCTCTGAAACCGCTCGCGCCCACTAGTTTCGGG 2520  
Db 2461 GCCCAAGGTATAGGTGCTTGTCTCTGAAACCGCTCGCGCCCACTAGTTTCGGG 2520  
QY 2521 GCGTATATGCTTAAGGCACATGTTATCGACCTTAACATCAGAACCGGGGTAGGACCATC 2580  
Db 2521 GCGTATATGCTTAAGGCACATGTTATCGACCTTAACATCAGAACCGGGGTAGGACCATC 2580  
QY 2581 ACCAAGGTCGCCCATCAGCTACTCCACCTATGGCAAGTTTCTTCCGCGGTTGCTGTC 2640  
Db 2581 ACCAAGGTCGCCCATCAGCTACTCCACCTATGGCAAGTTTCTTCCGCGGTTGCTGTC 2640  
QY 2641 TCTGGGGCGCTTATGACATCAATAATGATGATGAGTGCCACTCACTGACTCGACCACT 2700  
Db 2641 TCTGGGGCGCTTATGACATCAATAATGATGATGAGTGCCACTCACTGACTCGACCACT 2700  
QY 2701 ATCTGGGCATCGGCACAGTCTCGGACCAAGCGGAGCGCTGAGCGCGACTCGTCTGTC 2760  
Db 2701 ATCTGGGCATCGGCACAGTCTCGGACCAAGCGGAGCGCTGAGCGCGACTCGTCTGTC 2760  
QY 2761 CTGCGCACCGTACGCTCGGGATCGGTCACTGCGCAATCCAAACATCGAGGAGGTG 2820  
Db 2761 CTGCGCACCGTACGCTCGGGATCGGTCACTGCGCAATCCAAACATCGAGGAGGTG 2820  
QY 2821 GCTCTGTCCAGCTCGGAGAAATCCCTTTTATGGCAAGGCCATCCCATCGAGACCATC 2880  
Db 2821 GCTCTGTCCAGCTCGGAGAAATCCCTTTTATGGCAAGGCCATCCCATCGAGACCATC 2880



Db	5041	ACCACTGACAAAGTAAAGTGCCCGTGTCAAGTTCCGGCCCCCGAATTTCTTACAGAAAGTG	5100
Qy	5101	GATGGGGTCGGGTTCACAGGTACGCTCCAGCGTGCAAAACCCCTCCTACGGGAGAGGTC	5160
Db	5101	GATGGGGTCGGGTTCGCAAGGTACGCTCCAGCGTGCAAAACCCCTCCTAGGGAGAGGTC	5160
Qy	5161	ACATTCCTGGTCGGGCTCAATCAATACCTGTGGTGGGTCAAGCTCCCATGCGAGCCGAA	5220
Db	5161	ACATTCCTGGTCGGGCTCAATCAATACCTGTGGTGGGTCAAGCTCCCATGCGAGCCGAA	5220
Qy	5221	CCGACGTAGCAGTCTCCTCTGCGGAGGAGATCTCCCGCTCTTGGCGAGTCAATGACCTGAC	5280
Db	5221	CCGACGTAGCAGTCTCCTCTGCGGAGGAGATCTCCCGCTCTTGGCGAGTCAATGACCTGAC	5280
Qy	5281	GCTAAGCGTAGGCTGGCGAGGAGATCTCCCGCTCTTGGCGAGTCAATGACCTGAC	5340
Db	5281	GCTAAGCGTAGGCTGGCGAGGAGATCTCCCGCTCTTGGCGAGTCAATGACCTGAC	5340
Qy	5341	CTGTCTGGGCTCTCTTGAAGGCAACATGCACTACCCGTCATGACTCCCGGAGCGCTGAC	5400
Db	5341	CTGTCTGGGCTCTCTTGAAGGCAACATGCACTACCCGTCATGACTCCCGGAGCGCTGAC	5400
Qy	5401	CTCATCGAGGCAACCTCTCTGCGGAGGAGATGCGGCGGAGATGCGGCGGAGATGAG	5460
Db	5401	CTCATCGAGGCAACCTCTCTGCGGAGGAGATGCGGCGGAGATGCGGCGGAGATGAG	5460
Qy	5461	TCGAAATAAGGTAGTAATTTTGGACTCTTTCGAGCGGCTCCAAAGCGGAGGAGATGAG	5520
Db	5461	TCGAAATAAGGTAGTAATTTTGGACTCTTTCGAGCGGCTCCAAAGCGGAGGAGATGAG	5520
Qy	5521	AGGAAAGTATCCGTTCCGGCGGAGATCTTGGGAGGTCACAGAAATTCCTTCGAGCGATG	5580
Db	5521	AGGAAAGTATCCGTTCCGGCGGAGATCTTGGGAGGTCACAGAAATTCCTTCGAGCGATG	5580
Qy	5581	CCCATATGGGACCGCCGGATTACACCTTCCATCTGTAGAGTCTCGGAGGACCGCGAC	5640
Db	5581	CCCATATGGGACCGCCGGATTACACCTTCCATCTGTAGAGTCTCGGAGGACCGCGAC	5640
Qy	5641	TAGTCCTCTCCAGTGATACAGGGTGTCCATTTGCGGCTGCGAAGCGCCCTCCGATACCA	5700
Db	5641	TAGTCCTCTCCAGTGATACAGGGTGTCCATTTGCGGCTGCGAAGCGCCCTCCGATACCA	5700
Qy	5701	CCTCCAGGAGGAGGAGGAGTGTCTGTGCAAACTACCGGTGTCTTCTGCTTGGCG	5760
Db	5701	CCTCCAGGAGGAGGAGGAGTGTCTGTGCAAACTACCGGTGTCTTCTGCTTGGCG	5760
Qy	5761	GAGCTGCCACAAAGACTTTGCGAGCTCCGAACTCGTTCGAGTCTTCTGCTTGGCG	5820
Db	5761	GAGCTGCCACAAAGACTTTGCGAGCTCCGAACTCGTTCGAGTCTTCTGCTTGGCG	5820
Qy	5821	ACGGCTCTCTGACAGCCCTCCGAGAGCGGAGTCCGAGCTTGAAGTCTGAGTCTGATC	5880
Db	5821	ACGGCTCTCTGACAGCCCTCCGAGAGCGGAGTCCGAGCTTGAAGTCTGAGTCTGATC	5880
Qy	5881	TCTTCCATGCCCCCTTGAAGGAGGAGCGGAGTCCCGATCTCAGCAGCGGTCTTGG	5940
Db	5881	TCTTCCATGCCCCCTTGAAGGAGGAGCGGAGTCCCGATCTCAGCAGCGGTCTTGG	5940
Qy	5941	TCTTCCATGAGGAGGAGGAGTGTGAGGAGCGTCTGCTGCTGCTGCTTACATGAG	6000
Db	5941	TCTTCCATGAGGAGGAGGAGTGTGAGGAGCGTCTGCTGCTGCTGCTTACATGAG	6000
Qy	6001	ACAGGCGCTCTGATCAGCGCTGCGGAGGAGGAGTCCGATCTGAGTCTGAGTCTGATC	6060
Db	6001	ACAGGCGCTCTGATCAGCGCTGCGGAGGAGGAGTCCGATCTGAGTCTGAGTCTGATC	6060
Qy	6061	AGCAACTCTTTGCTCGGTCAACCACTTGGTCTATGCTACACATCTCGAGCGCAAGC	6120
Db	6061	AGCAACTCTTTGCTCGGTCAACCACTTGGTCTATGCTACACATCTCGAGCGCAAGC	6120
Qy	6121	CTCGGCGAGGAGGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG	6180
Db	6121	CTCGGCGAGGAGGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG	6180
Qy	6181	GTGCTCAAGGAGATGAAAGCGGCTCCACAGTTAAAGCTTAACTTCTATCCGTGGAG	6240
Db	6181	GTGCTCAAGGAGATGAAAGCGGCTCCACAGTTAAAGCTTAACTTCTATCCGTGGAG	6240
Qy	6241	GAAAGCTTAAAGCTGACGCCGCCCACTTCGCGCAGATCTAAATTTGGCTATGGGCGCAAG	6300
Db	6241	GAAAGCTTAAAGCTGACGCCGCCCACTTCGCGCAGATCTAAATTTGGCTATGGGCGCAAG	6300
Qy	6301	GACGTCCGAAACCTTATCCAGCAAGCGGCTTAAACCACTCCGCTCGTGGAGGACTTG	6360
Db	6301	GACGTCCGAAACCTTATCCAGCAAGCGGCTTAAACCACTCCGCTCGTGGAGGACTTG	6360
Qy	6361	CTGGAAGACACTGAGACACCAATTTGACACCACTATCATGGCAAAATGAGTTTCTGC	6420
Db	6361	CTGGAAGACACTGAGACACCAATTTGACACCACTATCATGGCAAAATGAGTTTCTGC	6420
Qy	6421	GTCCAAACAGAGAGGAGGCGGCAAGCGCTGCGCTTATCGATTTATCCAGATTTGGG	6480
Db	6421	GTCCAAACAGAGAGGAGGCGGCAAGCGCTGCGCTTATCGATTTATCCAGATTTGGG	6480
Qy	6481	GTTCTGTGTGCGAGAAATGGCCCTTTTACGATGTGTCTCCACCTCCCTCAGGCCGTG	6540
Db	6481	GTTCTGTGTGCGAGAAATGGCCCTTTTACGATGTGTCTCCACCTCCCTCAGGCCGTG	6540
Qy	6541	ATGGGCTCTTTCATACGATTTCCAAATCTCTCTGCGACAGCGGTCGAGTTCTCGTGAAT	6600
Db	6541	ATGGGCTCTTTCATACGATTTCCAAATCTCTCTGCGACAGCGGTCGAGTTCTCGTGAAT	6600
Qy	6601	GCCTGGAAGCGAAGAAATGCCCTTATGGGCTTCCCATATGACCCCGCTGTTTGAATCA	6660
Db	6601	GCCTGGAAGCGAAGAAATGCCCTTATGGGCTTCCCATATGACCCCGCTGTTTGAATCA	6660
Qy	6661	ACGCTCACTGAGAAATGATCCGCTGTTGAGAGTCAATCTACCAATGTTGAGTCTGAGC	6720
Db	6661	ACGCTCACTGAGAAATGATCCGCTGTTGAGAGTCAATCTACCAATGTTGAGTCTGAGC	6720
Qy	6721	CCGGAAGCGAGACAGCCATTAAGGTCCTCACAGAGCGGCTTACATCGGGGGCCCCCTG	6780
Db	6721	CCGGAAGCGAGACAGCCATTAAGGTCCTCACAGAGCGGCTTACATCGGGGGCCCCCTG	6780
Qy	6781	ACTAATTTTAAAGGCGAAGAACTGCGGCTATTCGCGGTGCGCGAGCGGTGACTGACG	6840
Db	6781	ACTAATTTTAAAGGCGAAGAACTGCGGCTATTCGCGGTGCGCGAGCGGTGACTGACG	6840
Qy	6841	ACCAGCTGCGGTAAATACCTCTCAATGTTTGAAGCGCGCTGCGGCTGTCGAGCTGCG	6900
Db	6841	ACCAGCTGCGGTAAATACCTCTCAATGTTTGAAGCGCGCTGCGGCTGTCGAGCTGCG	6900
Qy	6901	AAGCTCCAGGACTGCGAGGCTGCTGATGCGGAGACGACCTTGTGTTTCTGTAAGC	6960
Db	6901	AAGCTCCAGGACTGCGAGGCTGCTGATGCGGAGACGACCTTGTGTTTCTGTAAGC	6960
Qy	6961	GCGGGAGCCCAAGAGGACGAGGCGAGCTACGGGCTTCAACGAGGCTATGACTAGATAC	7020
Db	6961	GCGGGAGCCCAAGAGGACGAGGCGAGCTACGGGCTTCAACGAGGCTATGACTAGATAC	7020
Qy	7021	TCTGCCCCCTTGGGAGCCCGCCCAACAGAAATACGACTTGGAGTTGATAATCATGTC	7080
Db	7021	TCTGCCCCCTTGGGAGCCCGCCCAACAGAAATACGACTTGGAGTTGATAATCATGTC	7080
Qy	7081	TCTTCCAAATGTGTCAGTCCGCGGAGTGTATGCGGAGGAGGAGTGTATCTATCAGCCGT	7140
Db	7081	TCTTCCAAATGTGTCAGTCCGCGGAGTGTATGCGGAGGAGGAGTGTATCTATCAGCCGT	7140
Qy	7141	GACCCCAACACCCCTTGGCGGCTGCGTGGGAGACAGCTAGACACCTCCAGTCAAT	7200
Db	7141	GACCCCAACACCCCTTGGCGGCTGCGTGGGAGACAGCTAGACACCTCCAGTCAAT	7200
Qy	7201	TCTGCTAGGCAACATCATGATGCGGCCACCTTGTGGGCAAGGATGATCTCTGATG	7260
Db	7201	TCTGCTAGGCAACATCATGATGCGGCCACCTTGTGGGCAAGGATGATCTCTGATG	7260

QY 7261 ACTCATTTCTTCTCCATCTTCTAGCTCAGGAACAACCTTTGAAAAGAGCCCTAGATTGTGAG 7320  
DB |||||||  
QY 7261 ACTCATTTCTTCTCCATCTTCTAGCTCAGGAACAACCTTTGAAAAGAGCCCTAGATTGTGAG 7320  
DB |||||||  
QY 7321 ATCTACGGGGGCTGTACTTCCATTGAGCCACTTGACCTACCTCAGATCATTTCAACGACTC 7380  
DB |||||||  
QY 7321 ATCTACGGGGGCTGTACTTCCATTGAGCCACTTGACCTACCTCAGATCATTTCAACGACTC 7380  
DB |||||||  
QY 7381 CATGCCCTTAGCGCATTTTCACTCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT 7440  
DB |||||||  
QY 7381 CATGCCCTTAGCGCATTTTCACTCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT 7440  
DB |||||||  
QY 7441 TCATCCCTCAGGAACCTTGGGCTAGCGCTTGGCCAGTCTGAGACATCGGCCAGAAAGT 7500  
DB |||||||  
QY 7441 TCATCCCTCAGGAACCTTGGGCTAGCGCTTGGCCAGTCTGAGACATCGGCCAGAAAGT 7500  
DB |||||||  
QY 7501 GTCCGGCTTAGGCTACTGTGCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACTCTTTC 7560  
DB |||||||  
QY 7501 GTCCGGCTTAGGCTACTGTGCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACTCTTTC 7560  
DB |||||||  
QY 7561 AACTGGGAGTAGGACCAAGCTCAAACTCACTCCAACTCCCGCTGCGTCCCGATTGGAT 7620  
DB |||||||  
QY 7561 AACTGGGAGTAGGACCAAGCTCAAACTCACTCCAACTCCCGCTGCGTCCCGATTGGAT 7620  
DB |||||||  
QY 7621 TTATCCAGCTGTTCCTGCTGTTACAGGGGGAGAGACATATATCACAGCCCTGTCTCGT 7680  
DB |||||||  
QY 7621 TTATCCAGCTGTTCCTGCTGTTACAGGGGGAGAGACATATATCACAGCCCTGTCTCGT 7680  
DB |||||||  
QY 7681 GCCCGACCCCGCTGTTCTATGTTGTCCTACTCTCTACTTTCTGAGGGGTAGGCATCTAT 7740  
DB |||||||  
QY 7681 GCCCGACCCCGCTGTTCTATGTTGTCCTACTCTCTACTTTCTGAGGGGTAGGCATCTAT 7740  
DB |||||||  
QY 7741 CTACTCCCAACCGATGAAGGGGAGCTAAACTCCAGCCCAATAGGCCATCTCTTTT 7800  
DB |||||||  
QY 7741 CTACTCCCAACCGATGAAGGGGAGCTAAACTCCAGCCCAATAGGCCATCTCTTTT 7800  
DB |||||||  
QY 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860  
DB |||||||  
QY 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860  
DB |||||||  
QY 7861 TTTTCTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920  
DB |||||||  
QY 7861 TTTTCTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920  
DB |||||||  
QY 7921 TAGCTGTGAAGTCCGTGAGCCGCTGACTGAGAGAGTCTGATCTAGTCTGCTCTCTGC 7980  
DB |||||||  
QY 7921 TAGCTGTGAAGTCCGTGAGCCGCTGACTGAGAGAGTCTGATCTAGTCTGCTCTCTGC 7980  
DB |||||||  
QY 7981 AGATCAAGTACT 7992  
DB |||||||  
QY 7981 AGATCAAGTACT 7992  
DB |||||||

RESULT 4  
AD:283762  
ID ADC83762 standard; DNA; 10690 BP.  
XX AC ADC83762;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE pHCVNeol7.wt plasmid containing an HCV bicistronic replicon.  
XX  
KW Hepatitis C virus; thiosemicarbazone;  
KW 4-(cinnamyl)oxy)benzaldehyde thiosemicarbazone; RHEPLISA; Ia; hepatitis C;  
KW HCV replication system; bicistronic RNA replicon;  
KW neomycin phosphotransferase; human hepatoma cell line; Huh-7;  
KW neomycin sulphate; G418; pHCVNeol7.wt; replicon I37neo/NS3-3'/wt.;  
KW hepatotropic; virucide; antiinflammatory; ds.  
XX  
OE Synthetic.  
OE Unidentified.  
OE Hepatitis C virus.

XX US2003176503-A1.  
PN 18-SEP-2003.  
XX  
PD  
XX 19-APR-2002; 2002US-00125920.  
PF  
XX 20-APR-2001; 2001US-0285195P.  
PR  
XX (ALTA/) ALTAMURA S.  
PA (KOCH/) KOCH U.  
XX  
PI Altamura S, Koch U;  
XX WPI; 2003-778475/73.  
XX  
PT Use of thiosemicarbazone compounds for e.g. treating and preventing  
PT hepatitis C or its related condition, and delaying the onset of hepatitis  
PT C or its related condition.  
XX  
PS Example 3; SEQ ID NO 1; 30pp; English.  
XX  
CC The invention discloses a method for the treatment and prevention of  
CC hepatitis C, or its related condition, which involves the administration  
CC of thiosemicarbazone compounds, or its salts. The inhibitory activity of  
CC 4-(cinnamyl)oxy)benzaldehyde thiosemicarbazone was evaluated using  
CC RHEPLISA assay in a 96-well microplate format. The route of  
CC administration is oral, parenteral (e.g. subcutaneous, intravenous,  
CC intramuscular, intrasternal injection, or infusion), by inhalation spray  
CC e.g. 4-(cinnamyl)oxy)benzaldehyde thiosemicarbazone (Ia). The compounds  
CC are useful for treating and preventing hepatitis C or its related  
CC condition, delaying the onset of hepatitis C or its related condition and  
CC inhibiting replication of the hepatitis C virus. The compounds are potent  
CC inhibitor of replication of the hepatitis C virus. HCV replication  
CC systems can be obtained using various techniques. Selection of cells  
CC capable of supporting HCV replication can be achieved using bicistronic  
CC RNA replicons expressing a selectable marker, the neomycin  
CC phosphotransferase. Transfection of these replicons in the human hepatoma  
CC cell line, Huh-7, followed by cultivation in the presence of neomycin  
CC sulphate (G418), permits the isolation of clones that support HCV  
CC replication. The sequence presented is the pHCVNeol7.wt plasmid which  
CC contains the cDNA coding for an HCV bicistronic replicon identical to  
CC replicon I37neo/NS3-3'/wt.  
XX  
SQ Sequence 10690 BP; 2334 A; 3045 C; 2908 G; 2403 T; 0 U; 0 Other;  
Query Match 100.0%; Score 7992; DB 10; Length 10690;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 7992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCCAGCCCCCGATTGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAACACTG 60  
DB 1 GCCAGCCCCCGATTGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAACACTG 60  
QY 61 TCTTACGCAGAAAAGCGTCTAGCCATGGCGCTTATAGTATAGTGTGTCGACCTCCAGGAC 120  
DB 61 TCTTACGCAGAAAAGCGTCTAGCCATGGCGCTTATAGTATAGTGTGTCGACCTCCAGGAC 120  
QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGAAACCGGTGAGTACACCGGAATTGCGAG 180  
DB 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGAAACCGGTGAGTACACCGGAATTGCGAG 180  
QY 181 GAGACCGGGTCTCTTTTCTTGGATCAACCCCGCTCAATGCTCGGAGATTGGGGGTGCCCCC 240  
DB 181 GAGACCGGGTCTCTTTTCTTGGATCAACCCCGCTCAATGCTCGGAGATTGGGGGTGCCCCC 240  
QY 241 GCAGACTGCTAGCCGAGTGTGTGGTCCGAAAGCGCTTGTGCTACTGCTCCCTGATAGG 300  
DB 241 GCAGACTGCTAGCCGAGTGTGTGGTCCGAAAGCGCTTGTGCTACTGCTCCCTGATAGG 300  
QY 301 GTGCTTCGAGTGCCTCCGGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCTAAAC 360  
DB |||||||

Db 301 GTGCTTGGAGTGGCCCCGGAGGTCTCGTAGACCGTGCACCATGAGCACGAATCTCTAAAC 360  
Qy 361 CTCAAGAAAAACCAAGGGCGCGCATGATTGAACAAGATGATTTGCACGAGGTTC 420  
Db 361 CTCAAGAAAAACCAAGGGCGCGCATGATTGAACAAGATGATTTGCACGAGGTTC 420  
Qy 421 CGGCGCTTGGGTGAGAGGCTATTTCGGCTATGACTGGGCAACAAGACAAATCGGCTGT 480  
Db 421 CGGCGCTTGGGTGAGAGGCTATTTCGGCTATGACTGGGCAACAAGACAAATCGGCTGT 480  
Qy 481 CTGATGCCCGGTGTTCGGCTGTTCAGCGCAGGGGCGCGGCTTCTTTTGTCAAGACG 540  
Db 481 CTGATGCCCGGTGTTCGGCTGTTCAGCGCAGGGGCGCGGCTTCTTTTGTCAAGACG 540  
Qy 541 ACTGTCCGGTGCCCTGAATGAACATGCAGAGCAGGCGAGCGGCTATCGTGGCTGGCA 600  
Db 541 ACTGTCCGGTGCCCTGAATGAACATGCAGAGCAGGCGAGCGGCTATCGTGGCTGGCA 600  
Qy 601 CGACGGGGTTCCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGACTGCG 660  
Db 601 CGACGGGGTTCCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGACTGCG 660  
Qy 661 TGCTATTGGGGAGAGTGCCGGGCGAGGATCTCCTGTCACTCACCTTGTCTGCGCGAGA 720  
Db 661 TGCTATTGGGGAGAGTGCCGGGCGAGGATCTCCTGTCACTCACCTTGTCTGCGCGAGA 720  
Qy 721 AAGTATCCATCATGGCTGATGCAATGCGCGGCTGCATACGCTTGATCGGCTACCTGCC 780  
Db 721 AAGTATCCATCATGGCTGATGCAATGCGCGGCTGCATACGCTTGATCGGCTACCTGCC 780  
Qy 781 CATTCGACCAACAAGCGAAAATCGCATCGAGCGAGCACGTA CTGGAATGGAAGCGGTC 840  
Db 781 CATTCGACCAACAAGCGAAAATCGCATCGAGCGAGCACGTA CTGGAATGGAAGCGGTC 840  
Qy 841 TTGTGATCAGATGATCTGACGAAGAGCATCAGGGGCTCGCGCAGCCGAACTGTTCG 900  
Db 841 TTGTGATCAGATGATCTGACGAAGAGCATCAGGGGCTCGCGCAGCCGAACTGTTCG 900  
Qy 901 CAGGCTCAAGCGCGCATGCCGATGCCGAGGATCTCGTGTGACCCATGCGCATGCT 960  
Db 901 CAGGCTCAAGCGCGCATGCCGAGGAGATCTCGTGTGACCCATGCGCATGCT 960  
Qy 961 GTTTCGGAATCATGGTGGAAAATGGCGCTTTCTGGAATTCATCGACTGTGGCGGG 1020  
Db 961 GTTTCGGAATCATGGTGGAAAATGGCGCTTTCTGGAATTCATCGACTGTGGCGGG 1020  
Qy 1021 TGGGTGCGGACCGCTATCAGACATAGGGTGGCTACCGGTGATTTGCTGAAGAGC 1080  
Db 1021 TGGGTGCGGACCGCTATCAGACATAGGGTGGCTACCGGTGATTTGCTGAAGAGC 1080  
Qy 1081 TTGGCGGGAATGGGCTGACCGCTTCCTCGTGTCTTACGGTATCGCGCTCCCGATTGCG 1140  
Db 1081 TTGGCGGGAATGGGCTGACCGCTTCCTCGTGTCTTACGGTATCGCGCTCCCGATTGCG 1140  
Qy 1141 AGGCAATCGGCTTATCGGCTTCTGACGAGTTCCTGAGTTTAAACAGACCAACG 1200  
Db 1141 AGGCAATCGGCTTATCGGCTTCTGACGAGTTCCTGAGTTTAAACAGACCAACG 1200  
Qy 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCTCCCGCTAACGTTCTGGC 1260  
Db 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCTCCCGCTAACGTTCTGGC 1260  
Qy 1261 CGAAGCGCTTGAATGAAGCGGCTGTGCTGTCTATATGTTATTTTCCACCATATTG 1320  
Db 1261 CGAAGCGCTTGAATGAAGCGGCTGTGCTGTCTATATGTTATTTTCCACCATATTG 1320  
Qy 1321 CGGCTTTTGGCAATGTAGGGGCGGAAACCTGGCTGTCTTCTTGAAGAGCATTCCT 1380  
Db 1321 CGGCTTTTGGCAATGTAGGGGCGGAAACCTGGCTGTCTTCTTGAAGAGCATTCCT 1380  
Qy 1381 AGGGGTCTTCCCTCTCGCAAGGATGCAAGGTCTGTGTAATGCTGTGAAGGAGCA 1440  
Db 1381 AGGGGTCTTCCCTCTCGCAAGGATGCAAGGTCTGTGTAATGCTGTGAAGGAGCA 1440

Qy 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACAAGCTCTGTAGCAGCCCTTTGCAAGGACGG 1500  
Db 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACAAGCTCTGTAGCAGCCCTTTGCAAGGACGG 1500  
Qy 1501 AACCCCCACCTGGCGACAGGTGCTCTGCGGCAAAAGCCACGTTAAGATACACT 1560  
Db 1501 AACCCCCACCTGGCGACAGGTGCTCTGCGGCAAAAGCCACGTTAAGATACACT 1560  
Qy 1561 GCAAGGGCGGCAACAACCCAGTGCACAGTTGTGAGTTGGAATGTTGTAAGAGAGTCAAA 1620  
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Db 1621 TGGCTCTCTCAAGGCTATTCAACAAGGGCTGAAGGATGCCCAAGGTACCCCATTTG 1680  
Qy 1681 ATGGATCTGATCTGGGCTCTCGGTGCACATGCTTTACATGTTTGTAGTTCGAGGTTAAA 1740  
Db 1681 ATGGATCTGATCTGGGCTCTCGGTGCACATGCTTTACATGTTTGTAGTTCGAGGTTAAA 1740  
Qy 1741 AACGTCTAGGCCCCCGAACCAACCGGGAAGTGGTTTCTTTGAAAAACACGATAATACC 1800  
Db 1741 AACGTCTAGGCCCCCGAACCAACCGGGAAGTGGTTTCTTTGAAAAACACGATAATACC 1800  
Qy 1801 ATGGGCTTATAGGCTCTATCCCAACAGACGCGAGGCTACTTGGCTGCATCATCACT 1860  
Db 1801 ATGGGCTTATAGGCTCTATCCCAACAGACGCGAGGCTACTTGGCTGCATCATCACT 1860  
Qy 1861 AGCTTCACAGCCCGGACAGAACCCAGTCCAGGGGAGGTCCAAAGTGTCTTCCACCGCA 1920  
Db 1861 AGCTTCACAGCCCGGACAGAACCCAGTCCAGGGGAGGTCCAAAGTGTCTTCCACCGCA 1920  
Qy 1921 ACACAATCTTCTGGGCACTCGTCAATGGCGCTGTGTTGGAGTGTCTATCATGTGTGCC 1980  
Db 1921 ACACAATCTTCTGGGCACTCGTCAATGGCGCTGTGTTGGAGTGTCTATCATGTGTGCC 1980  
Qy 1981 GGCTCAAGAGCCCTTGGCGGCAACAGGGGCAATCAACCAATGTATCAACAAATGTGAGC 2040  
Db 1981 GGCTCAAGAGCCCTTGGCGGCAACAGGGGCAATCAACCAATGTATCAACAAATGTGAGC 2040  
Qy 2041 CAGGACCTCGTGGCTGGCAAGSCCCCCCGGGCGGCTTCCCTGACACCAATGACCTGCG 2100  
Db 2041 CAGGACCTCGTGGCTGGCAAGSCCCCCCGGGCGGCTTCCCTGACACCAATGACCTGCG 2100  
Qy 2101 GGCACTCGACCTTTACTTGGTCAAGGATCGCGATGTCTATCCGGTGGCGCGGCGG 2160  
Db 2101 GGCACTCGACCTTTACTTGGTCAAGGATCGCGATGTCTATCCGGTGGCGCGGCGG 2160  
Qy 2161 GGCGACAGAGGGGAGCTACTCTCCCGAGGCGCTCTCTACTTTGAAGGGCTCTTCG 2220  
Db 2161 GGCGACAGAGGGGAGCTACTCTCCCGAGGCGCTCTCTACTTTGAAGGGCTCTTCG 2220  
Qy 2221 GGCGCTCCACTGTCTGCGGCAAGCTGTGGGCACTCTTCCGGGCTGCGGTGTC 2280  
Db 2221 GGCGCTCCACTGTCTGCGGCAAGCTGTGGGCACTCTTCCGGGCTGCGGTGTC 2280  
Qy 2281 ACCGAGGGGTTCGGAAGGCGGTGAGCTTTGTACCGCTCGAGTCTATGGAACCACTATG 2340  
Db 2281 ACCGAGGGGTTCGGAAGGCGGTGAGCTTTGTACCGCTCGAGTCTATGGAACCACTATG 2340  
Qy 2341 CGGTCCCGGTCTTACAGGACAACTGTCCTCCCGAGGCGCTCTCTACTTTGAAGGGTCTTCG 2400  
Db 2341 CGGTCCCGGTCTTACAGGACAACTGTCCTCCCGAGGCGCTCTCTACTTTGAAGGGTCTTCG 2400  
Qy 2401 GCCCATCTACAGCCCTACTGTAGCGGCAAGACACTAAGGTGCGGCTGGTATGCA 2460  
Db 2401 GCCCATCTACAGCCCTACTGTAGCGGCAAGACACTAAGGTGCGGCTGGTATGCA 2460  
Qy 2461 GCCCAAGGGTATAAGGTGCTTGTCTTGAACCCCGTCCGCGCCACCTTAGGTTTCGGG 2520  
Db 2461 GCCCAAGGGTATAAGGTGCTTGTCTTGAACCCCGTCCGCGCCACCTTAGGTTTCGGG 2520



Dd	4681	ACGGTGTGACGATTTCAAGACCTGGCTCCAGTCCAAAGCTCCTCGCGGATTTGCGGGA	4740	Qy	5821	ACGGCTCTCTGACGACGCCCTCCGACGACGCGGATCCGACCTTGAGTGTGAC	5880
Qy	4741	GTCCCTTCTTCTCATGTCAAGTGGGTACAAAGGAGTCTGGCGGGGACGCGCATCATG	4800	Dd	5821	ACGGCTCTCTCTGACGACGCCCTCCGACGACGCGGATCCGACCTTGAGTGTGAC	5880
Dd	4741	GTCCCTTCTTCTCATGTCAAGTGGGTACAAAGGAGTCTGGCGGGGACGCGCATCATG	4800	Qy	5881	TCCTCATGCCCCCTTTGAGGGGAGCCGGGGATCCCGATCTCAGCGACGGGTCTTGG	5940
Qy	4801	CAAAACACCTGCGCATGTGGAGCAGATCAACGGACATGTGAAAAAGCGTTTCCATGAGG	4860	Dd	5881	TCCTCATGCCCCCTTTGAGGGGAGCCGGGGATCCCGATCTCAGCGACGGGTCTTGG	5940
Dd	4801	CAAAACACCTGCGCATGTGGAGCAGATCAACGGACATGTGAAAAAGCGTTTCCATGAGG	4860	Qy	5941	TCTACCGTAAGCAGGAGGCTAGTAGGACGCTGCTGCTCGATGCTCTACACATGG	6000
Qy	4861	ATCGTGGGCGCTAGGACCTGTAGTAACACGCTGGCATGGAACATTCCTTAAACCGGTAC	4920	Dd	5941	TCTACCGTAAGCAGGAGGCTAGTAGGACGCTGCTGCTCGATGCTCTACACATGG	6000
Dd	4861	ATCGTGGGCGCTAGGACCTGTAGTAACACGCTGGCATGGAACATTCCTTAAACCGGTAC	4920	Qy	6001	ACAGCGCCCTGATCACGCCATGCGCTCGGAGGAAACCAAGCTCCCATTAATGCACTG	6060
Qy	4921	ACCAAGGCGCCCTGACACCCCTCCCGCGCGCAAAATTTATCTAGGGCGCTGTGGCGGGTG	4980	Dd	6001	ACAGCGCCCTGATCACGCCATGCGCTCGGAGGAAACCAAGCTCCCATTAATGCACTG	6060
Dd	4921	ACCAAGGCGCCCTGACACCCCTCCCGCGCGCAAAATTTATCTAGGGCGCTGTGGCGGGTG	4980	Qy	6061	AGCAACTCTTTGCTCCGTCACCAAACTTGTCTATGCTACAACTCTCGACGCGCAAGC	6120
Qy	4981	GCTGCTGAGGAGTACGTGGAGTTAGCGGGTGGGGATTTCCACTAGCTGACGGGCATG	5040	Dd	6061	AGCAACTCTTTGCTCCGTCACCAAACTTGTCTATGCTACAACTCTCGACGCGCAAGC	6120
Dd	4981	GCTGCTGAGGAGTACGTGGAGTTAGCGGGTGGGGATTTCCACTAGCTGACGGGCATG	5040	Qy	6121	CTGGGCGAAGAGGCTCACCTTTGACAGACTGCGAGTCTCTGGACGACCACTACCGGAC	6180
Qy	5041	ACCACTGACAAAGTAAAGTCCCGTGTCAAGTTCCGGCCCGGAAATTTCTAGGGCGCTG	5100	Dd	6121	CTGGGCGAAGAGGCTCACCTTTGACAGACTGCGAGTCTCTGGACGACCACTACCGGAC	6180
Dd	5041	ACCACTGACAAAGTAAAGTCCCGTGTCAAGTTCCGGCCCGGAAATTTCTAGGGCGCTG	5100	Qy	6181	GTGCTCAAGGAGATCAAGGCGAAGCGCTTGAAGGCTTAACTTCTATCCGTGGAG	6240
Qy	5101	GATGGGTCGGTGTGACAGGTACGCTCAGCGTGCAGGCTGCAAGCCCTCTACGGGAGGATC	5160	Dd	6181	GTGCTCAAGGAGATCAAGGCGAAGCGCTTGAAGGCTTAACTTCTATCCGTGGAG	6240
Dd	5101	GATGGGTCGGTGTGACAGGTACGCTCAGCGTGCAGGCTGCAAGCCCTCTACGGGAGGATC	5160	Qy	6241	GAAGCTGTAGCTGAGCGCCCACTTGGGCGAGATCTAAATTTGGCTATGGGCGCAAG	6300
Qy	5161	ACATTCCTGGTGGGCTCAATCAATACCTGTGGTCAAGTCCCATGCGAGCCGAA	5220	Dd	6241	GAAGCTGTAGCTGAGCGCCCACTTGGGCGAGATCTAAATTTGGCTATGGGCGCAAG	6300
Dd	5161	ACATTCCTGGTGGGCTCAATCAATACCTGTGGTCAAGTCCCATGCGAGCCGAA	5220	Qy	6301	GACGTCGGAACCTTATCCAGCAAGCGCTTAAACCACTCCGCTCGGTGGAAGGACTTG	6360
Qy	5221	CCGACCTGAGCAGTGTCACTTCCATGCTCACCGACCCCTCCCACTTACCGCGGAGACG	5280	Dd	6301	GACGTCGGAACCTTATCCAGCAAGCGCTTAAACCACTCCGCTCGGTGGAAGGACTTG	6360
Dd	5221	CCGACCTGAGCAGTGTCACTTCCATGCTCACCGACCCCTCCCACTTACCGCGGAGACG	5280	Qy	6361	CTGGAAGACACTGAGACCACTTGAACACCACTATGCGCAACCAATATGAGGTTTCTGC	6420
Qy	5281	GCTAAGCGTAGGCTGGCGAGGGATCTCCCGCTCTTGGCGAGCTCATCAGCTAGCCAG	5340	Dd	6361	CTGGAAGACACTGAGACCACTTGAACACCACTATGCGCAACCAATATGAGGTTTCTGC	6420
Dd	5281	GCTAAGCGTAGGCTGGCGAGGGATCTCCCGCTCTTGGCGAGCTCATCAGCTAGCCAG	5340	Qy	6421	GTCCAAACAGAGAGGGGGCGCAAGCAGCTCGCTTATCGTATTCGCAAGTTTCTGC	6480
Qy	5341	CTGCTCGGCTTCTTGAAGGCAACATGCACTACCGGTCAAGTCCCGGACGCTGAC	5400	Dd	6421	GTCCAAACAGAGAGGGGGCGCAAGCAGCTCGCTTATCGTATTCGCAAGTTTCTGC	6480
Dd	5341	CTGCTCGGCTTCTTGAAGGCAACATGCACTACCGGTCAAGTCCCGGACGCTGAC	5400	Qy	6481	GTTCGTGTGCGAGAAAATGGGCTTTACGATGTGTCTCCACCTCTCCAGGCGGTG	6540
Qy	5401	CTCATCGAGGCAACCTCCTGTGGCGCAGGAGATGGCGGACATCACCCCGGTGGAG	5460	Dd	6481	GTTCGTGTGCGAGAAAATGGGCTTTACGATGTGTCTCCACCTCTCCAGGCGGTG	6540
Dd	5401	CTCATCGAGGCAACCTCCTGTGGCGCAGGAGATGGCGGACATCACCCCGGTGGAG	5460	Qy	6541	ATGGGCTCTTTCATACGATTCGATCTCTCTGGACAGCGGCTCGAGTTCTCGTGAAT	6600
Qy	5461	TCAGAAATAGGTAGTAAATTTTGGACTCTTTGAGCGCTTCCAGCGGCTCCAGCGGAGGATGAG	5520	Dd	6541	ATGGGCTCTTTCATACGATTCGATCTCTCTGGACAGCGGCTCGAGTTCTCGTGAAT	6600
Dd	5461	TCAGAAATAGGTAGTAAATTTTGGACTCTTTGAGCGCTTCCAGCGGCTCCAGCGGAGGATGAG	5520	Qy	6601	GCCTGGAACGAGAAATGCCCTATGGGCTTCGCAATGACACCCGCTGTTTGACTCA	6660
Qy	5521	AGGAGTATCCGTCGGCGGAGATCTCGGAGGTCGAGAAATTCCTTCGAGCGATG	5580	Dd	6601	GCCTGGAACGAGAAATGCCCTATGGGCTTCGCAATGACACCCGCTGTTTGACTCA	6660
Dd	5521	AGGAGTATCCGTCGGCGGAGATCTCGGAGGTCGAGAAATTCCTTCGAGCGATG	5580	Qy	6661	ACGGTCACTGAGAAATGACATTCCTGTGTGAGGAGTCAATCTACCAATGTTGAGTGGCC	6720
Qy	5581	CCCATATGGGACGCGCGGATTAACACCTTCCACTGTAGAGTCCCTGAGAGGACCGGAC	5640	Dd	6661	ACGGTCACTGAGAAATGACATTCCTGTGTGAGGAGTCAATCTACCAATGTTGAGTGGCC	6720
Dd	5581	CCCATATGGGACGCGCGGATTAACACCTTCCACTGTAGAGTCCCTGAGAGGACCGGAC	5640	Qy	6721	CCGGAAGCCAGACAGGCGCATAGGTCGCTCACAGAGCGGCTTTACATCGGGGCGCCCTG	6780
Qy	5641	TAGCTCCTCCAGTGTACACGGGTGTCCATTTGCGGCTCCGAGGCGCTCCGATACCA	5700	Dd	6721	CCGGAAGCCAGACAGGCGCATAGGTCGCTCACAGAGCGGCTTTACATCGGGGCGCCCTG	6780
Dd	5641	TAGCTCCTCCAGTGTGTACACGGGTGTCCATTTGCGGCTCCGAGGCGCTCCGATACCA	5700	Qy	6781	ACTAATTTAAAGGGCAGAACTGCGGCTATCGCGGTCGCGCGGAGCGGTGACTGACG	6840
Qy	5701	CCTCCAGGAGGAGGAGCGGTGTCTGTCAAGATCTACCGTGTCTCTGCTTGGCG	5760	Dd	6781	ACTAATTTAAAGGGCAGAACTGCGGCTATCGCGGTCGCGCGGAGCGGTGACTGACG	6840
Dd	5701	CCTCCAGGAGGAGGAGCGGTGTCTGTCAAGATCTACCGTGTCTCTGCTTGGCG	5760	Qy	6841	ACCAGTGTGGTAATACCTCTCATGTTACTTTGAAGGCGGCTCGGCGCTGTGAGTGTGG	6900
Qy	5761	GAGCTGCCACAAAGACCTTCGGAGCTCCGAAATCGTGGCGCTGTGAGTGTGG	5820	Dd	6841	ACCAGTGTGGTAATACCTCTCATGTTACTTTGAAGGCGGCTCGGCGCTGTGAGTGTGG	6900
Dd	5761	GAGCTGCCACAAAGACCTTCGGAGCTCCGAAATCGTGGCGCTGTGAGTGTGG	5820				

6901 AAGCTCCAGGACTGCACGATGCTCGTATGCGGAGACGACCTGTGCTTATCTGTGAAAGC 6960  
6901 AAGCTCCAGGACTGCACGATGCTCGTATGCGGAGACGACCTGTGCTTATCTGTGAAAGC 6960  
6961 GGGGGGACCCAGAGAGAGAGCGAGCGCTTACGGGCTTTCACGGAGGCTATGACTAGATAC 7020  
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7561 AACTGGCAGTAAGGACCAAGCTCAACTCACTCCATCCCGTGGTCCAGTTGGAT 7620  
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7621 TTATCCAGCTGGTTCGTTGCTGTTACAGGGGGGAGACATATATACAGCTGTCTCGT 7680  
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7681 GCCCGACCCCGCTGGTTCAATGTTGCTTACTCTTCTTCTGTTAGGGGTAGGATCTAT 7740  
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7861 TTTTTCCTTT 7920  
7861 TTTTTCCTTT 7920  
7921 TAGCTGTGAAGGTCGGTGAAGCGCTTCACTGCAGAGAGTGTCTGATACTGCGCTCTCTGC 7980  
7921 TAGCTGTGAAGGTCGGTGAAGCGCTTCACTGCAGAGAGTGTCTGATCTGCGCTCTCTGC 7980  
7981 AGATCAAGTACT 7992

Db 7981 AGATCAAGTACT 7992  
RESULT 5  
ID AAL47281 standard; DNA; 7992 BP.  
XX AAL47281;  
AC AAL47281;  
XX 30-AUG-2002 (first entry)  
XX Hepatitis C virus sub-genomic replicon recombinant clone HCV24.  
XX Hepatitis; HCV; core-neo; NS3 proteinase/helicase; vaccine; diagnosis;  
XX virucide; hepatotropic; gene therapy; anti-viral; gene; ds.  
XX Hepatitis C virus.  
XX WO200238793-A2.  
XX 16-MAY-2002.  
XX 02-NOV-2001; 2001WO-US046350.  
XX 07-NOV-2000; 2000US-0245866P.  
XX (ANAD-) ANADYS PHARM INC.  
XX Bichko V;  
XX WPI; 2002-490082/52.  
XX Novel nucleic acid encoding replication competent recombinant hepatitis C  
XX virus genome useful for screening anti-hepatitis C virus therapeutics and  
XX for vaccine development.  
XX Claim 11; Page 70-75; 85pp; English.  
XX The present invention provides protein and coding sequences from  
XX Hepatitis C virus (HCV), comprising all or part of the HCV genome and  
XX able to replicate efficiently when transfected into a susceptible cell  
XX line without reducing the growth rate of the cell line by more than 10  
XX fold. The sequences are useful for screening for anti-HCV therapeutics,  
XX for detecting antibodies to HCV in a biological sample such as blood,  
XX serum, plasma, blood cells, lymphocytes, or liver cells from a subject,  
XX for deriving authentic HCV components such as replication-competent non-  
XX infectious, replication-defective infection-component, and replication-  
XX defective non-infectious HCV, in gene therapy or gene vaccination  
XX targeted to hepatic tissue for treating an animal infected or susceptible  
XX to HCV infection and for studying HCV infection and propagation. The  
XX present sequence is a clone of a fragment of the HCV genome designated  
XX HCV24  
XX  
SQ Sequence 7992 BP; 1648 A; 2369 C; 2242 G; 1733 T; 0 U; 0 Other;  
Query Match 100.0%; Score 7990.4; DB 6; Length 7992;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 GCCAGCCCCGATTGGGGGCGACACTCCACATAGATCACTCCCTCTGAGGAATCTG 60  
Db 1 GCCAGCCCCGATTGGGGGCGACACTCCACATAGATCACTCCCTCTGAGGAATCTG 60  
Qy 61 TCTTACGCGAGAAAGCGCTTAGCCATGGCGTTAGTATGATGCTGTCAGCTCCAGAC 120  
Db 61 TCTTACGCGAGAAAGCGCTTAGCCATGGCGTTAGTATGATGCTGTCAGCTCCAGAC 120  
Qy 121 CCCCCCTCCCGGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAG 180  
Db 121 CCCCCCTCCCGGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAG 180  
Qy 181 GACGACCGGGTCTTTTCTTGGATCAACCCGCTCAATGCTGGAGATTTGGGCGTGCCCC 240



2401 GCCCATCTACACGCCCTACTGTTAGCGGACAGACATAAGGTGCCGCTCGGTATGCA 2460  
2401 GCCCATCTACACGCCCTACTGTTAGCGGACAGACATAAGGTGCCGCTCGGTATGCA 2460  
2461 GCCCAAGGGTATAAGGTGCTGCTCTGAACCCGTCGTCGCCGCCACCCCTAGTGTTCGGG 2520  
2461 GCCCAAGGGTATAAGGTGCTGCTGAACCCGTCGTCGCCGCCACCCCTAGTGTTCGGG 2520  
2521 GCGTATATGTTAAGGCAATGGTATCGACCCCTAAATCAGAAACCGGGGTAAAGCAATC 2580  
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2581 ACCAGGGTCCCGCCATCAGGTACTCCACCTATGGCAAGTTCCTGCGGACGGTGTTCG 2640  
2581 ACCAGGGTCCCGCCATCAGGTACTCCACCTATGGCAAGTTCCTGCGGACGGTGTTCG 2640  
2641 TCTGGGGGCGCTATGACATCATATATGTAGTGGCACTCAACTGACTCGACCACT 2700  
2641 TCTGGGGGCGCTATGACATCATATATGTAGTGGCACTCAACTGACTCGACCACT 2700  
2701 ATCTGGGCACTGGCAAGTCTCTGACCAAGGGAGACGGCTGGAGCGGACTCGTCTG 2760  
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2821 GCTCTCTCAGCACTGGAGAAATCCCTTTTATGCGCAAGCCATCCCATCGAGACCACT 2880  
2881 AAGGGGGAGGACCTCATTTTCTGCAATTCCTCAAGAGAAATGTGATGAGCTCGCGCG 2940  
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2941 AAGCTGCGGCTCGGACTCAATGCTGTAGCATATTTACCGGGGCTTGTATGATCGTC 3000  
2941 AAGCTGCGGCTCGGACTCAATGCTGTAGCATATTTACCGGGGCTTGTATGATCGTC 3000  
3001 ATACCAACTAGCGGAGACGTCATTTGCTGTAGCAACCGACGCTCTAATGACGGGCTTACC 3060  
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3181 CAGCGGAGGACGAGCTGTTAGGGGAGGATGGGCAATTTACAGTTTGTGACTCCAGGA 3240  
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3241 GAACGGGCTCGGCACTGTTGATTCCTCGGTCTGTGCGAGTCTATGACGGGCTGT 3300  
3301 GCTTGTGACGACTCAGCGCGGACGACCTCAGTTAGTTTGGGGCTTACCTAAACACA 3360  
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3361 CCAGGGTGGCGGCTGCTGCCAGGACCACTGTGAGTCTTGGGAGAGGCTTTACAGGCTC 3420  
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3421 ACCACATAGACGCGCATTTCTGCGGAGTAAAGAGGAGGAGCACTTCCCTTAC 3480  
3421 ACCACATAGACGCGCATTTCTGCGGAGTAAAGAGGAGGAGCACTTCCCTTAC 3480

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3541 CAAATGTGGAAGTGTCTCATACGGCTAAAGCTACGCTGACGCGCCCAACGCCCTGCTG 3600  
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3661 ATGGCATGATCGGCTGACCTGGAGTCTGCAAGGACACCTGGTGTGTAGCGGA 3720  
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3781 ATCATCTTGTCCGGAAGCGGCCCATCATTTCCGACAGGGAAGTCTTTACCGGGAGTTC 3840  
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3841 GATGATGGAAGAGTGGCGCTCACACCTCCCTTACATCGAAGGGAATGCAAGTCCGC 3900  
3901 GACAAATTCAGAAAGGCAATCGGGTGTGCAAAAGCAGCCACCAAGCAAGCGGAGGCT 3960  
3901 GACAAATTCAGAAAGGCAATCGGGTGTGCAAAAGCAGCCACCAAGCAAGCGGAGGCT 3960  
3961 GCTGCTCCGCTGTTGGAATTCAGAGTGGCGGACCTCGAAGCCTTTCTGGGGAAGCATATG 4020  
3961 GCTGCTCCGCTGTTGGAATTCAGAGTGGCGGACCTCGAAGCCTTTCTGGGGAAGCATATG 4020  
4021 TGGAATTTGATCAGCGGGATACATATTTAGCAGGCTTGTCCACTCTGCTCCGCAACCCC 4080  
4021 TGGAATTTGATCAGCGGGATACATATTTAGCAGGCTTGTCCACTCTGCTCCGCAACCCC 4080  
4081 GCGATAGCATCACTGATGCGATTCACAGCTCTATCAGAGCCCGCTCAGCAGCATAGGCTTGG 4140  
4081 GCGATAGCATCACTGATGCGATTCACAGCTCTATCAGAGCCCGCTCAGCAGCATAGGCTTGG 4140  
4141 ACCCTCTGTTTAAACATCTCTGGGGGATGGGTGGCGCCCAACTTGTCTCTCCAGGCT 4200  
4141 ACCCTCTGTTTAAACATCTCTGGGGGATGGGTGGCGCCCAACTTGTCTCTCCAGGCT 4200  
4201 GCTTCTGCTTGTAGCGCGGCTCGCTGGAGCGGCTGTGGCAGCATAGGCTTGGG 4260  
4201 GCTTCTGCTTGTAGCGCGGCTCGCTGGAGCGGCTGTGGCAGCATAGGCTTGGG 4260  
4261 AAGGTGCTTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGGCTGCTGGCC 4320  
4261 AAGGTGCTTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGGCTGCTGGCC 4320  
4321 TTTAAGGTCTAGCGCGGAGATGCCCTCCACCGAGGACCTGGTTAACTCTCCCTGCT 4380  
4321 TTTAAGGTCTAGCGCGGAGATGCCCTCCACCGAGGACCTGGTTAACTCTCCCTGCT 4380  
4381 ATCTCTCTCCCTTGGCGGCTAGTCTGGGGTGTGGCGCAGCATAGCTCGGCGAC 4440  
4381 ATCTCTCTCCCTTGGCGGCTAGTCTGGGGTGTGGCGCAGCATAGCTCGGCGAC 4440  
4441 GTGGGCGCAGGGAGGGGCTGTGCACTGGATGAACCGGCTGTAGCGTTCCGTTCCGGG 4500  
4441 GTGGGCGCAGGGAGGGGCTGTGCACTGGATGAACCGGCTGTAGCGTTCCGTTCCGGG 4500  
4501 GGTAAACCAAGTCTCCCCCAGCACTATGTGCTGAGAGCGCTGAGAGCAGTGTCACT 4560  
4501 GGTAAACCAAGTCTCCCCCAGCACTATGTGCTGAGAGCGCTGAGAGCAGTGTCACT 4560  
4561 CAGATCTCTCTAGTCTTACCATCACTCAGTCTGTGGAAGGGCTTACCACTGGATCAAC 4620

Db	4561	CAGATCCCTCTAGTCTTTACCACTCACTCAGCTGCTGAAGAGCCTTCACCATGTGATCAAC	4620
QY	4621	GAGGACTGCTCCACGCCATGCTCCGGCTCGTGGCTTAAGAGATGTTTGGGATTTGATATGC	4680
Db	4621	GAGGACTGCTCCACGCCATGCTCCGGCTCGTGGCTTAAGAGATGTTTGGGATTTGATATGC	4680
QY	4681	ACGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGTCTCTGCCGCGATTCGCCGGA	4740
Db	4681	ACGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGTCTCTGCCGCGATTCGCCGGA	4740
QY	4741	GTCCCTCTTCTCATGTCAACGTGGGTACAGGAGGAGCTCTGGCGGGGGACGGCATCATG	4800
Db	4741	GTCCCTCTTCTCATGTCAACGTGGGTACAGGAGGAGCTCTGGCGGGGGACGGCATCATG	4800
QY	4801	CAAACCACTGCCCCATGTGGAGCACAGATCAACCGGACATGTGAAAAACGGTTCATCAGG	4860
Db	4801	CAAACCACTGCCCCATGTGGAGCACAGATCAACCGGACATGTGAAAAACGGTTCATCAGG	4860
QY	4861	ATCGTGGGGCCTAGGACCTGTAGTAAACAGTGGGATGGAACATTTCCCCATTAACGCGTAC	4920
Db	4861	ATCGTGGGGCCTAGGACCTGTAGTAAACAGTGGGATGGAACATTTCCCCATTAACGCGTAC	4920
QY	4921	ACCACGGCCCCCTGCACGCCCTCCCCGGCGCCAAATTTATTTAGGGCGCTGTGGCGGGTG	4980
Db	4921	ACCACGGCCCCCTGCACGCCCTCCCCGGCGCCAAATTTATTTAGGGCGCTGTGGCGGGTG	4980
QY	4981	GCTGCTGAGGAGTAGCTGGAGGTTACGGGGTGGGGGATTTCCACTACGTGACGGGCATG	5040
Db	4981	GCTGCTGAGGAGTAGCTGGAGGTTACGGGGTGGGGGATTTCCACTACGTGACGGGCATG	5040
QY	5041	ACCACTGACACGTAAAGTGCCCGTGTGAGTTCCCGCCCCCGAAATTTCTTCACAGAAGTG	5100
Db	5041	ACCACTGACACGTAAAGTGCCCGTGTGAGTTCCCGCCCCCGAAATTTCTTCACAGAAGTG	5100
QY	5101	GATGGGTGGGTTGTCACAGTACGCTCCAGCGTGCNAACCCCTCTCTACGGGAGGAGTTC	5160
Db	5101	GATGGGTGGGTTGTCACAGTACGCTCCAGCGTGCNAACCCCTCTCTACGGGAGGAGTTC	5160
QY	5161	ACATTCCTGTGGGCTCAATCAATCACTGTTGGGTACAGCTCCCATGCGGACCGCGAA	5220
Db	5161	ACATTCCTGTGGGCTCAATCAATCACTGTTGGGTACAGCTCCCATGCGGACCGCGAA	5220
QY	5221	CCGACGTAGAGTGCTCACTTCATGCTCAACGACCCCTCCACATTAACGGCGGAGACG	5280
Db	5221	CCGACGTAGAGTGCTCACTTCATGCTCAACGACCCCTCCACATTAACGGCGGAGACG	5280
QY	5281	GCTAAGCGTAGGCTGGCCAGGGATCTCCCCCTCTTGGCAGCTCATCAGTACGCAG	5340
Db	5281	GCTAAGCGTAGGCTGGCCAGGGATCTCCCCCTCTTGGCAGCTCATCAGTACGCAG	5340
QY	5341	CTGTCTGCGCTTCTTTGAAGGCACATGACCTACCCGTCATGACTCCCCGGACGCTGAC	5400
Db	5341	CTGTCTGCGCTTCTTTGAAGGCACATGACCTACCCGTCATGACTCCCCGGACGCTGAC	5400
QY	5401	CTCATGAGGCGAACCTCTGTGGCGGAGAGATGGGCGGGAAACATCAACCCGCTGGAG	5460
Db	5401	CTCATGAGGCGAACCTCTGTGGCGGAGAGATGGGCGGGAAACATCAACCCGCTGGAG	5460
QY	5461	TCAGAAAAAAGCTAGTATTTTGGACTCTTTCGAGCCGCTCCAGCGGAGGAGATGAG	5520
Db	5461	TCAGAAAAAAGCTAGTATTTTGGACTCTTTCGAGCCGCTCCAGCGGAGGAGATGAG	5520
QY	5521	AGGGAAGTATCCGTTCCGGCGGAGATCTTCGAGGCTCCAGGAATTCCTTCGAGGATG	5580
Db	5521	AGGGAAGTATCCGTTCCGGCGGAGATCTTCGAGGCTCCAGGAATTCCTTCGAGGATG	5580
QY	5581	CCCATATGGGCACGCCCGGATTAACACCCCTCCACTGTTAGAGTCTCTGGAAGGACCCGAC	5640
Db	5581	CCCATATGGGCACGCCCGGATTAACACCCCTCCACTGTTAGAGTCTCTGGAAGGACCCGAC	5640
QY	5641	TACGTCCCTCCAGTGTACACGGGTGTCATTTGCGGCTGTCAGAGGCCCTCCGATACCA	5700

Db	5641	TACGTCCTCCAGTGGTACACGGGTGTCCATTGCCGCTGCGCAAGCGCCCTCCGATACCA	5700
Qy	5701	CCTCCAGGAGGAGACAGACGGTTGTCTGTTCAGAAATCTACCGTGTCTTCTGCTTGGGG	5760
Db	5701		
Qy	5761	GAGTCGCGCCACAAAGACCTTCGGCAGCTCCGAATCGTCGGCGTGCAGACAGCGCGACGGCA	5820
Db	5761	GAGTCGCGCCACAAAGACCTTCGGCAGCTCCGAATCGTCGGCGTGCAGACAGCGCGACGGCA	5820
Qy	5821	ACGCGCTCTCTGACCGAGCCCTCCGACGACGGCGACGGGATCCGAGTTCGAGTCGTAC	5880
Db	5821	ACGCGCTCTCTGACCGAGCCCTCCGACGACGGCGACGGGATCCGAGTTCGAGTCGTAC	5880
Qy	5881	TCCTCCATGCCCCCTTTGAGGGGAGCGGGGGATCCGATCTCAGCAGCGGTCCTGG	5940
Db	5881	TCCTCCATGCCCCCTTTGAGGGGAGCGGGGGATCCGATCTCAGCAGCGGTCCTGG	5940
Qy	5941	TCTACCGTAAGCGAGGAGGTAGTGAGGACGTCTGCTGCTGCTCGATCTCTACACATGG	6000
Db	5941	TCTACCGTAAGCGAGGAGGTAGTGAGGACGTCTGCTGCTGCTCGATCTCTACACATGG	6000
Qy	6001	ACAGCGCCCTGATCACGCCATGCGCTCGGAGGAAACCAAGCTGCCCATCAATGCATG	6060
Db	6001	ACAGCGCCCTGATCACGCCATGCGCTCGGAGGAAACCAAGCTGCCCATCAATGCATG	6060
Qy	6061	AGCAACTCTTTGCTCCGTACCAACAACTTGCTGTATGTCTACAAATCTCGCAGCGCAAGC	6120
Db	6061	AGCAACTCTTTGCTCCGTACCAACAACTTGCTGTATGTCTACAAATCTCGCAGCGCAAGC	6120
Qy	6121	CTGCGGAGAAAGGTACCTTTGACAGACTCGAGGTCTTGAGCAGCCACTACCGGAC	6180
Db	6121	CTGCGGAGAAAGGTACCTTTGACAGACTCGAGGTCTTGAGCAGCCACTACCGGAC	6180
Qy	6181	GTCTCAAGGAGATGAGGCGAAGGCTCCACAGTTAAGGCTAACTTCTATCCGTGGAG	6240
Db	6181	GTCTCAAGGAGATGAGGCGAAGGCTCCACAGTTAAGGCTAACTTCTATCCGTGGAG	6240
Qy	6241	GAAGCTGTAAGCTGACGCGCCACACATTCGGCCAGATCTAAATTTGGCTATGGGGCAAG	6300
Db	6241	GAAGCTGTAAGCTGACGCGCCACACATTCGGCCAGATCTAAATTTGGCTATGGGGCAAG	6300
Qy	6301	GAGTCGCGAAACCTATCCAGCAAGGCGTTAACCATCCGCTCCGTGTGGAAGCACTTG	6360
Db	6301	GAGTCGCGAAACCTATCCAGCAAGGCGTTAACCATCCGCTCCGTGTGGAAGCACTTG	6360
Qy	6361	CTGGAAGACACTGAGACACCAATGACCAACCATCATGCGCAAAAATGAGGTTTTCTGC	6420
Db	6361	CTGGAAGACACTGAGACACCAATGACCAACCATCATGCGCAAAAATGAGGTTTTCTGC	6420
Qy	6421	GTCCAAACAGAAAGGGGGCGCAAGCGCTGCTTATCGTATTCAGATTCGCGG	6480
Db	6421	GTCCAAACAGAAAGGGGGCGCAAGCGCTGCTTATCGTATTCAGATTCGCGG	6480
Qy	6481	GTTCGTGTGCGAAGAAATGGCCCTTTACGATGTGGTCTCCACCTCCTCAGGCGGTG	6540
Db	6481	GTTCGTGTGCGAAGAAATGGCCCTTTACGATGTGGTCTCCACCTCCTCAGGCGGTG	6540
Qy	6541	ATGGGCTCTTCATACGGATTCCAATACTCTCTCGGACAGGGGTCCAGTTCCTGGTAAT	6600
Db	6541	ATGGGCTCTTCATACGGATTCCAATACTCTCTCGGACAGGGGTCCAGTTCCTGGTAAT	6600
Qy	6601	GCTCGAAAGCGAAGAAATGCCCTATGGGCTTCGCATATGACACCGCTGTTTTGACTCA	6660
Db	6601	GCTCGAAAGCGAAGAAATGCCCTATGGGCTTCGCATATGACACCGCTGTTTTGACTCA	6660
Qy	6661	ACGGTCACTGAGATGACATCCGTGTGAGGAGTCAATCTACCAATGTTGTGACTTGGCC	6720
Db	6661	ACGGTCACTGAGATGACATCCGTGTGAGGAGTCAATCTACCAATGTTGTGACTTGGCC	6720
Qy	6721	CCGGAAGCGACAGGCCATAGGTCGTTCACAGAGCGGCTTATCATCGGGGCCCCCTG	6780
Db	6721	CCGGAAGCGACAGGCCATAGGTCGTTCACAGAGCGGCTTATCATCGGGGCCCCCTG	6780



XX Claim 16; Page; 69pp; English.  
XX  
CC The invention relates to nucleic acid molecules comprising altered HCV  
CC NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)  
CC internal ribosome entry site (IRES) region coding for one or more NS3,  
CC NS5A, or EMCV IRES mutations, respectively. The location of the mutations  
CC are detailed in the specification. Also included are (1) an expression  
CC vector comprising a nucleotide sequence coding for the altered nucleic  
CC acids, which is transcriptionally coupled to an exogenous promoter; (2) a  
CC recombinant cell human hepatoma cell comprising the altered nucleic acids  
CC ; (3) a recombinant cell produced by introducing into a human hepatoma  
CC cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)  
CC replicon enhanced cell or which containing a functional HCV replicon; (5)  
CC an HCV replicon enhanced cells made in the method; and (6) measuring the  
CC ability of a compound to affect HCV activity. The HCV replicons and HCV  
CC expression, and HCV and host cell interactions, producing HCV RNA and  
CC proteins, and providing a system for measuring the ability of a compound  
CC to modulate one or more HCV activities e.g. to discover drugs which may  
CC treat HCV mediated diseases such as liver failure, cirrhosis and  
CC hepatocellular carcinoma. The present sequence is an HCV based vector  
CC pHCNeo.17 mutant of the invention. Note: The present sequence is not  
CC shown in the specification but was created by the indexer using the HCV  
CC vector sequence appearing as ABK91412 and the information in Claim 16  
XX  
SQ Sequence 10690 BP; 2335 A; 3045 C; 2907 G; 2403 T; 0 U; 0 Other;

Query Match 100.0%; Score 7990.4; DB 6; Length 10690;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCAGCCCCCGATTGGGGGCGACACTCCACATAGATCACTCCCTCTGGAGAACTACTG 60  
DB 1 GCCAGCCCCCGATTGGGGGCGACACTCCACATAGATCACTCCCTCTGGAGAACTACTG 60

QY 61 TCTTCCAGCAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTCAGCCCTCCAGGAC 120  
DB 61 TCTTCCAGCAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTCAGCCCTCCAGGAC 120

QY 121 CCCCCCTCCCGGAGAGCCATAGTGGTCTCGGNAACCGGTGAGTACACCGGAATTGCCAG 180  
DB 121 CCCCCCTCCCGGAGAGCCATAGTGGTCTCGGNAACCGGTGAGTACACCGGAATTGCCAG 180

QY 181 GACGACCGGTCTCTTCTTGATCAACCCCGCTCAATGCCCTGGAGATTGGCGCTGCCCC 240  
DB 181 GACGACCGGTCTCTTCTTGATCAACCCCGCTCAATGCCCTGGAGATTGGCGCTGCCCC 240

QY 241 GCGAGACTGTAGCCGAGTAGTGTGGGTCCGAAAGGCCTTGTGGTACTGCTGATAGG 300  
DB 241 GCGAGACTGTAGCCGAGTAGTGTGGGTCCGAAAGGCCTTGTGGTACTGCTGATAGG 300

QY 301 GTCTTTGCGAGTCCCGGGAGGTCTCGTAGACCGTGACCATGAGCAGCAATCTTAAAC 360  
DB 301 GTCTTTGCGAGTCCCGGGAGGTCTCGTAGACCGTGACCATGAGCAGCAATCTTAAAC 360

QY 361 CTCAAGAGAAAAACCAAGGCGCGCCATGATTGAACAAGATGATGTCAGCGAGGTCTC 420  
DB 361 CTCAAGAGAAAAACCAAGGCGCGCCATGATTGAACAAGATGATGTCAGCGAGGTCTC 420

QY 421 CGGCGCTTTGGTGGAGAGCTATTTCGGCTATGACTGGGCACACAGACAATCGGCTGCT 480  
DB 421 CGGCGCTTTGGTGGAGAGCTATTTCGGCTATGACTGGGCACACAGACAATCGGCTGCT 480

QY 481 CTGATCCGCGCTGTTCCGCTCTAGCGCAGGGGCGCCGGTCTTTTGTCAAGACCG 540  
DB 481 CTGATCCGCGCTGTTCCGCTCTAGCGCAGGGGCGCCGGTCTTTTGTCAAGACCG 540

QY 541 ACTGTCCGCTGCTGAACTGAATCGAGGACGAGGACGCGGCTATCGTGGCTGGCCA 600  
DB 541 ACTGTCCGCTGCTGAACTGAATCGAGGACGAGGACGCGGCTATCGTGGCTGGCCA 600

QY 601 CGAGCGGCGTTCCTTGGCAGCTGTGCTCGAGCTTGTCTACTGAAGCGGGAAGGACTGGC 660

DB 601 CGAGCGGCGTTCCTTGGCAGCTGTGCTCGAGCTTGTCTACTGAAGCGGGAAGGACTGGC 660

QY 661 TGCATTATGGGCGAAAGTGCAGGAGTCTCTGTCTATCTCACCTTCTCTCTCCGCGAGA 720  
DB 661 TGCATTATGGGCGAAAGTGCAGGAGTCTCTGTCTATCTCACCTTCTCTCTCCGCGAGA 720

QY 721 AAGTATCCATCCATCGCTGATGCAATGGGCGGCTGCATACGCTTGATCCGGTACTCTGCC 780  
DB 721 AAGTATCCATCCATGGCTGATGCAATGGGCGGCTGCATACGCTTGATCCGGTACTCTGCC 780

QY 781 CATTCGACCAACAAGCGAAACATCGCATCGAGCAGCAGTACTCGGATGGAAGCCGGTC 840  
DB 781 CATTCGACCAACAAGCGAAACATCGCATCGAGCAGCAGTACTCGGATGGAAGCCGGTC 840

QY 841 TTGTGATCAGGATGATCTGGACGAAGCATCAGGGGCTCGCGCCAGCCGAACTGTTTCG 900  
DB 841 TTGTGATCAGGATGATCTGGACGAAGCATCAGGGGCTCGCGCCAGCCGAACTGTTTCG 900

QY 901 CCAGGCTCAAGGCGCGCATGCCCCGAGGAGTCTGCTGTGACCCATGGCGATGCTT 960  
DB 901 CCAGGCTCAAGGCGCGCATGCCCCGAGGAGTCTGCTGTGACCCATGGCGATGCTT 960

QY 961 GCTTGGCGAATATCATGCTGGAATAATGCGCGCTTTTCTGGATTCTATCGACTGTGCGCGC 1020  
DB 961 GCTTGGCGAATATCATGCTGGAATAATGCGCGCTTTTCTGGATTCTATCGACTGTGCGCGC 1020

QY 1021 TGGTGTGGCGGACCGCTATCAGGACATAGCTTGGCTTACCGGTGATTTGCTGAAGAGC 1080  
DB 1021 TGGTGTGGCGGACCGCTATCAGGACATAGCTTGGCTTACCGGTGATTTGCTGAAGAGC 1080

QY 1081 TTGGCGCGAATGGGCTGACCGCTTCTCTGCTTTTACGCTATCGCGCTTCCCGATTGCG 1140  
DB 1081 TTGGCGCGAATGGGCTGACCGCTTCTCTGCTTTTACGCTATCGCGCTTCCCGATTGCG 1140

QY 1141 AGCGCATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCACAACG 1200  
DB 1141 AGCGCATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCACAACG 1200

QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCTTCTCCCTTCCCTCCCTCCCTCCCTTACTTGGC 1260  
DB 1201 GTTTCCTCTAGCGGATCAATTCGCGCTTCTCCCTTCCCTCCCTCCCTTACTTGGC 1260

QY 1261 CGAAGCGCTTGAATAGCGCGGTGCTGCTTGTCTATATGATTTTCCACCATTTG 1320  
DB 1261 CGAAGCGCTTGAATAGCGCGGTGCTGCTTGTCTATATGATTTTCCACCATTTG 1320

QY 1321 CCGTCTTTTGGCAATGTGAGGCGCCGGAACCTTGGCGCTTCTTCTTGACGAGCATTCCT 1380  
DB 1321 CCGTCTTTTGGCAATGTGAGGCGCCGGAACCTTGGCGCTTCTTCTTGACGAGCATTCCT 1380

QY 1381 AGGGGTCTTTCCTCTCGCCAAAGGAATGCAAGTCTGTTGAATGTGCTGAAGGAGCA 1440  
DB 1381 AGGGGTCTTTCCTCTCGCCAAAGGAATGCAAGTCTGTTGAATGTGCTGAAGGAGCA 1440

QY 1441 GTTTCCTCTGAGAGTCTTGAAGACAAACAACTGTGTAGCGACCTTTGCGAGCGCGG 1500  
DB 1441 GTTTCCTCTGAGAGTCTTGAAGACAAACAACTGTGTAGCGACCTTTGCGAGCGCGG 1500

QY 1501 AACCCGCCACCTTGGCGACAGGTGCTTGGCGCAAAAGCCAGCTGTATAAGGATACACCT 1560  
DB 1501 AACCCGCCACCTTGGCGACAGGTGCTTGGCGCAAAAGCCAGCTGTATAAGGATACACCT 1560

QY 1561 GCAGAGCGCGCAACACCCAGTGCACGTTGTGAGTTGATAGTTGTGGAAGAGTCAAA 1620  
DB 1561 GCAGAGCGCGCAACACCCAGTGCACGTTGTGAGTTGATAGTTGTGGAAGAGTCAAA 1620

QY 1621 TGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGGATGCCAGAGGATGCCCATTTGT 1680  
DB 1621 TGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGGATGCCAGAGGATGCCCATTTGT 1680

QY 1681 ATGGGATCTGATCTGGGCGCTCGGTGCAATGCTTTACATGTTGTAGTCGAGGTTAAA 1740



QY	3901	GAACAATTCAAACAGAGAGGCANATCGGGTTGCTGCAAAACAGCCACCAAGCAACGAGCGAGGCT	3960
Db	3901	GAACAATTCAAACAGAGAGCAATCGGGTTGCTGCAAAACAGCCACCAAGCAACGAGCGAGGCT	3960
QY	3961	GCTGCTCCCGTGGTGGAAATCCAAGTGGCGGACCTTCGAAGCCTTCTGCGGCGAAGCATATG	4020
Db	3961	GCTGCTCCCGTGGTGGAAATCCAAGTGGCGGACCTTCGAAGCCTTCTGCGGCGAAGCATATG	4020
QY	4021	TGGAATTTCAATCAGCGGGATACAATATTTAGCAGGCTTGTCCAATCTGCTGCTGGCAACCCC	4080
Db	4021	TGGAATTTCAATCAGCGGGATACAATATTTAGCAGGCTTGTCCAATCTGCTGCTGGCAACCCC	4080
QY	4081	GGGATAGCATCACTGATGGCAATTCACAGCCTCTATACAGGCCGCTCACCACCCAAAT	4140
Db	4081	GGGATAGCATCACTGATGGCAATTCACAGCCTCTATACAGGCCGCTCACCACCCAAAT	4140
QY	4141	ACCCTCTCTTTTAAACATCCTGGGGGATGGGTGGCGGCCCAACTTGTCTCTCCAGCGCT	4200
Db	4141	ACCCTCTCTTTTAAACATCCTGGGGGATGGGTGGCGGCCCAACTTGTCTCTCCAGCGCT	4200
QY	4201	GCTTCTGCTTTTCGTAGGCGCGGCATCGCTGGAGCGGCTGTTGGCAGCATAGAGCCTTGGG	4260
Db	4201	GCTTCTGCTTTTCGTAGGCGCGGCATCGCTGGAGCGGCTGTTGGCAGCATAGAGCCTTGGG	4260
QY	4261	AAGGTGCTTGTGGATATTTTGGCAGGTTATGGACAGGGGTGGCAGCGCGCTCGTGGCC	4320
Db	4261	AAGGTGCTTGTGGATATTTTGGCAGGTTATGGACAGGGGTGGCAGCGCGCTCGTGGCC	4320
QY	4321	TTTAAAGGTCATAGCGGCGAGATGCCCTCCACCGAGAACCTGGTTAACTTCTCCCTGCT	4380
Db	4321	TTTAAAGGTCATAGCGGCGAGATGCCCTCCACCGAGAACCTGGTTAACTTCTCCCTGCT	4380
QY	4381	ATCCTCTCCCTGGCGCCCTAGTCTCGGGGTCGTGTGCGCAGCGATCTAGCTGTGGCGAC	4440
Db	4381	ATCCTCTCCCTGGCGCCCTAGTCTCGGGGTCGTGTGCGCAGCGATCTAGCTGTGGCGAC	4440
QY	4441	GTGGGCCCCAGGGAGGGGGCTGTGCATGGATGAACCGCGTGATAGCGTTTCGCTTCGCG	4500
Db	4441	GTGGGCCCCAGGGAGGGGGCTGTGCATGGATGAACCGCGTGATAGCGTTTCGCTTCGCG	4500
QY	4501	GGTAAACACAGTCTCCCCACGCATATGTCCCTGAGAGCAGCCTCGAGCATGTGTCACT	4560
Db	4501	GGTAAACACAGTCTCCCCACGCATATGTCCCTGAGAGCAGCCTCGAGCATGTGTCACT	4560
QY	4561	CAGATCCTCTCTAGTCTTTACCATCACTCAGCTCTGTAAGAGGCTTCACAGTGGATCAAC	4620
Db	4561	CAGATCCTCTCTAGTCTTTACCATCACTCAGCTCTGTAAGAGGCTTCACAGTGGATCAAC	4620
QY	4621	GAGGACTGCTCCAGCCCATGCTCGGCTCTGGCTTAAGAGATGTTTGGGATGGATATGC	4680
Db	4621	GAGGACTGCTCCAGCCCATGCTCGGCTCTGGCTTAAGAGATGTTTGGGATGGATATGC	4680
QY	4681	ACGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAGTCTCTGCGCGGATTCGCGGGA	4740
Db	4681	ACGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAGTCTCTGCGCGGATTCGCGGGA	4740
QY	4741	GTCCCTTCTTCTCATGTCTCAACGTGGGTACAAGGAGTCTGGCGGGCGCAGCGCATATG	4800
Db	4741	GTCCCTTCTTCTCATGTCTCAACGTGGGTACAAGGAGTCTGGCGGGCGCAGCGCATATG	4800
QY	4801	CAAAACCTGCCCCATGTGGAGCACAGATCACCGGACATGTGAAAAACGGTTTCCATGAGG	4860
Db	4801	CAAAACCTGCCCCATGTGGAGCACAGATCACCGGACATGTGAAAAACGGTTTCCATGAGG	4860
QY	4861	ATCGTGGGGCTTAGGACCTGTAGTAAACGTGGCATGGAACTTCCCAATTAAACGCGTAC	4920
Db	4861	ATCGTGGGGCTTAGGACCTGTAGTAAACGTGGCATGGAACTTCCCAATTAAACGCGTAC	4920
QY	4921	ACCAACGGGCCCTTGACAGCCCTCCCCGGCGCCAAATTTATTTAGGGCGCTGTGGCGGTG	4980
Db	4921	ACCAACGGGCCCTTGACAGCCCTCCCCGGCGCCAAATTTATTTAGGGCGCTGTGGCGGTG	4980
QY	4981	GCTGCTAGAGATGATCGTGAGGTTACGCGGGTGGGGATTTTCCACTAGCTGACGGGCAATG	5040

4981	GCTGCTCAGAGATGCTGTGGAGGTTACGCGGTCGGGGGATTTCCACTACGTGACGGGCATG	5040
5041	ACCACTGACAACGTAAGTAGTCCCGTGTCAAGTTCTCCGGCCCCCGAAATCTTTCACAGAAGTG	5100
5041	ACCACTGACAACGTAAGTAGTCCCGTGTCAAGTTCTCCGGCCCCCGAAATCTTTCACAGAAGTG	5100
5101	GATGGGTGCGGTTGCA CAGGTACGCTCCAGCGTGCAGAACCCCTCTTACGGGAGGAGGTC	5160
5101	GATGGGTGCGGTTGCA CAGGTACGCTCCAGCGTGCAGAACCCCTCTTACGGGAGGAGGTC	5160
5161	ACATTCTGCTGCTCGGCTCAATCAATACCTGTGGTGTCA CAGTCCCATTCGAGGCCGAA	5220
5161	ACATTCTGCTGCTCGGCTCAATCAATACCTGTGGTGTCA CAGTCCCATTCGAGGCCGAA	5220
5221	CCGGAAGTACAGTGTCTACTTCATGCTCACCGACCCCTCCCAANTATCGGCGGAGACG	5280
5221	CCGGAAGTACAGTGTCTACTTCATGCTCACCGACCCCTCCCAANTATCGGCGGAGACG	5280
5281	GCTAAGGTAGGTCGCCAGGGGATCTCCGCCCTCTTCGGCCAGTCTACAGTACGCCAG	5340
5281	GCTAAGGTAGGTCGCCAGGGGATCTCCGCCCTCTTCGGCCAGTCTACAGTACGCCAG	5340
5341	CTGCTCTGCGCTTCTTTGAAGGCAATGCATACCCGTATGATCTCCCGGACGCTGAC	5400
5341	CTGCTCTGCGCTTCTTTGAAGGCAATGCATACCCGTATGATCTCCCGGACGCTGAC	5400
5401	CTCATCGAGCCCAACTCTGTGTGGCGGAGAGATGGCGGGAAATCACCCGCTGGAG	5460
5401	CTCATCGAGCCCAACTCTGTGTGGCGGAGAGATGGCGGGAAATCACCCGCTGGAG	5460
5461	TCAGAAAAAAGGTAGTAAATTTTGACTCTTTTCGAGCCGCTCCAAAGCGGAGGAGTACG	5520
5461	TCAGAAAAAAGGTAGTAAATTTTGACTCTTTTCGAGCCGCTCCAAAGCGGAGGAGTACG	5520
5521	AGGGAAGTATCCGTTTCGGCGGAGATCTGCGGAGGTTCAGAAATTCCTTCGAGCGATG	5580
5521	AGGGAAGTATCCGTTTCGGCGGAGATCTGCGGAGGTTCAGAAATTCCTTCGAGCGATG	5580
5581	CCCATATGGGCAAGCCCGGATTTACAAACCTTCACACTGTTAGTCTCTGGAAGGACCCGAC	5640
5581	CCCATATGGGCAAGCCCGGATTTACAAACCTTCACACTGTTAGTCTCTGGAAGGACCCGAC	5640
5641	TACGTCCTCTCAGTGTGTACAGGGGTGTCCATTGCGCGCTGCAAGGCCCTCCGATACCA	5700
5641	TACGTCCTCTCAGTGTGTACAGGGGTGTCCATTGCGCGCTGCAAGGCCCTCCGATACCA	5700
5701	CTTCCACGGAGGAAGACGAGTGTCTGTCTGATGAAATCTACCGTGTCTTTCGCTTGCGG	5760
5701	CTTCCACGGAGGAAGACGAGTGTCTGTCTGATGAAATCTACCGTGTCTTTCGCTTGCGG	5760
5761	GAGCTCGCCACAAAGACCTTCGGCAGCTCCGAATCTGTCGGCGTTCGACAGGGGACCGCA	5820
5761	GAGCTCGCCACAAAGACCTTCGGCAGCTCCGAATCTGTCGGCGTTCGACAGGGGACCGCA	5820
5821	ACGGCCTCTCTGACACGACCTTCGACAGCGGACCGGGATCCCGATCTCAGCGTGTAGTCTGAC	5880
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5881	TCCTCCATGCCGCCCTTGTAGGGGAGCCGGGGATCCCGATCTCAGCGAGCGGTCTTGG	5940
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5941	TCTACCGTAAAGGAGGAGGTAGTGGAGGTCTGCTGCTGCTGATGTCCTTACATGG	6000
6001	ACAGGCGCCTGATACAGCCATGCGCTGCGGAGGAAACCAAGCTGCCCATCAATGCACTG	6060
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6121 CTGGGCGAAGAGGTCACCTTTGACAGACTGACAGTCTCTGGACGACACTACCGGAC 6180  
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6181 GTGCTCAAGGAGATCAAGCGAGGCTCCACAGTTAAGGCTAAACTCTTATCCGTGGAG 6240  
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6481 GTTCGTGTGCGAGAAATGCGCTTTACGATGTTGCTCCACCTCCCTCAGGCGG 6540  
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7981 AGATCAAGTACT 7992

## RESULT 7

ABK91435  
ID ABK91435 standard; DNA; 10690 BP.

XX ABK91435;

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

DE Hepatitis C virus vector construct pHVNeo.17m2.

XX HCV; ss; pHVNeo.17m2; adaptive mutation; liver failure; cirrhosis;  
KW hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;  
KW internal ribosome entry site; IRES; NS5A; HCV replication; mutant.  
XX Hepatitis C virus.

OS Encephalomyocarditis virus.  
OS Escherichia coli.  
OS Enterobacteria phage T7.  
OS Synthetic.

OS Key Location/Qualifiers  
FH 5'UTR 1..341  
FT /\*tag= a  
FT CDS 342..1181  
FT /\*tag= b  
FT /product= "Core-neo fusion protein"  
FT misc\_signal 1190..1800  
FT /\*tag= c  
FT /label= IRES  
FT /note= "Internal ribosome entry site from ECWV"  
FT CDS 1801..7758  
FT /\*tag= d  
FT /product= "Polyprotein"  
FT /note= "Comprising NS3, NS4A, NS4B, NS5A and NS5B"  
FT mutation replace(5243,C)  
FT /\*tag= e  
FT 3'UTR 7759..7991  
FT /\*tag= f  
FT misc\_feature 7992..10690  
FT /\*tag= g  
FT /note= "Plasmid derived sequences"

XX WO200259321-A2.

XX 01-AUG-2002.

XX 16-JAN-2002; 2002WO-EP000526.

XX 23-JAN-2001; 2001US-0263479P.

XX (RICE-) 1ST RICERCHIE BIOL MOLECOLARE ANGELETTI.

XX De Francesco R, Migliaccio G, Paonessa G;

XX WPI; 2002-599793/64.

XX New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV  
XX NS3 encoding region, or encephalomyocarditis virus (EMCV) internal  
XX ribosome entry site (IRES) region, useful in studying HCV replication and  
XX expression.

XX Claim 16; Page; 69pp; English.

XX The invention relates to nucleic acid molecules comprising altered HCV  
XX NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)  
XX internal ribosome entry site (IRES) region coding for one or more NS3,  
XX NS5A, or EMCV IRES mutations, respectively. The location of the mutations  
XX are detailed in the specification. Also included are (1) an expression  
XX vector comprising a nucleotide sequence coding for the altered nucleic  
XX acids, which is transcriptionally coupled to an exogenous promoter; (2) a  
XX recombinant cell human hepatoma cell comprising the altered nucleic acids  
XX ; (3) a recombinant cell produced by introducing into a human hepatoma  
XX cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)  
XX replicon enhanced cell or which containing a functional HCV replicon; (5)  
XX an HCV replicon enhanced cells made in the method; and (6) measuring the  
XX ability of a compound to affect HCV activity. The HCV replicons and HCV  
XX replicon enhanced cells are useful in studying HCV replication and  
XX expression, and HCV and host cell interactions, producing HCV RNA and  
XX proteins, and providing a system for measuring the ability of a compound  
XX to modulate one or more HCV activities e.g. to discover drugs which may  
XX treat HCV mediated diseases such as liver failure, cirrhosis and  
XX hepatocellular carcinoma. The present sequence is an HCV based vector  
XX pHCvneo.17 mutant of the invention. Note: The present sequence is not  
XX shown in the specification but was created by the indexer using the HCV  
XX vector sequence appearing as ABK91412 and the information in Claim 16

XX Sequence 10690 BP; 2334 A; 3044 C; 2908 G; 2404 T; 0 U; 0 Other;

Query Match 100.0%; Score 7990.4; DB 6; Length 10690;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	GCACGCCCGGATTTGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGAACTACTG	60
DB	1	GCACGCCCGGATTTGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGAACTACTG	60
QY	61	TCTTCACGAGAAAGCGTCTAGCCATGCGGTAGTATGAGTGTCTGTGAGCCTCCAGGAC	120
DB	61	TCTTCACGAGAAAGCGTCTAGCCATGCGGTAGTATGAGTGTCTGTGAGCCTCCAGGAC	120
QY	121	CCCCCTCCCGGAGAGCCATAGTGTCTGCGAACCGGTAGATACACGGAAATGCCAG	180
DB	121	CCCCCTCCCGGAGAGCCATAGTGTCTGCGAACCGGTAGATACACGGAAATGCCAG	180
QY	181	GACGACCGGGTCTTCTTTGGATCAACCCCGCTCAATGCTCGAGATTTGGGGCTGCCCCC	240
DB	181	GACGACCGGGTCTTCTTTGGATCAACCCCGCTCAATGCTCGAGATTTGGGGCTGCCCCC	240
QY	241	CGGAGACTGCTAGCCGAGTAGTGTGGTTCGCGAAAGCCCTTGTGTTACTGCTGATAGG	300
DB	241	CGGAGACTGCTAGCCGAGTAGTGTGGTTCGCGAAAGCCCTTGTGTTACTGCTGATAGG	300
QY	301	GTGCTTGGAGTGCCTCCGGGAGGTCTCTAGACCGTGCACCATGAGCAGAACTCTAAAC	360
DB	301	GTGCTTGGAGTGCCTCCGGGAGGTCTCTAGACCGTGCACCATGAGCAGAACTCTAAAC	360
QY	361	CTCAAGAAACCAAAAGGGCGGCCCATGATTGAACAAGATGGATTGCACGACGTTCTC	420
DB	361	CTCAAGAAACCAAAAGGGCGGCCCATGATTGAACAAGATGGATTGCACGACGTTCTC	420
QY	421	CGGCGCTTGGGTGGAGAGGCTATTCCGGCTATGACTGGGCAACAACAGCAATCGGCTCT	480
DB	421	CGGCGCTTGGGTGGAGAGGCTATTCCGGCTATGACTGGGCAACAACAGCAATCGGCTCT	480
QY	481	CTGATGCCGCGGTTCGCGCTGTCAGGCGAGGGGCGCGGTTCTTTTGTCAAGACCG	540
DB	481	CTGATGCCGCGGTTCGCGCTGTCAGGCGAGGGGCGCGGTTCTTTTGTCAAGACCG	540
QY	541	ACCTGTCCGGTGCCTGAACTGAACCTGACGACGAGGCGCGGCTATCGTGGCTGGCCA	600
DB	541	ACCTGTCCGGTGCCTGAACTGAACCTGACGACGAGGCGCGGCTATCGTGGCTGGCCA	600
QY	601	CGACGGCGTTCCTTTCGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGACTGGC	660
DB	601	CGACGGCGTTCCTTTCGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGACTGGC	660
QY	661	TGCTATTGGGCGAAGTCCCGGGCAGGATCTCTGTCTATCTACCTTGTCTCTCCGAGGA	720
DB	661	TGCTATTGGGCGAAGTCCCGGGCAGGATCTCTGTCTATCTACCTTGTCTCTCCGAGGA	720
QY	721	AAGTATCCATCATGCTGATGCAATCGCGGCTGCTAGCTTGTATCCGGTACCTGCTGC	780
DB	721	AAGTATCCATCATGCTGATGCAATCGCGGCTGCTAGCTTGTATCCGGTACCTGCTGC	780
QY	781	CATTTCACCAACGAGGAAACATCGCATCGAGCGACACGTAATCGGATGGAAGCGGTC	840
DB	781	CATTTCACCAACGAGGAAACATCGCATCGAGCGACACGTAATCGGATGGAAGCGGTC	840
QY	841	TTGTCGATCAGGATGATCGGAGAGCATCAGGGGCTCGGCGCCAGCCGAACTGTTCG	900
DB	841	TTGTCGATCAGGATGATCGGAGAGCATCAGGGGCTCGGCGCCAGCCGAACTGTTCG	900
QY	901	CCAGGCTCAAGGCGGCATGCGCGGAGGATCTCGTGTGACCCATGGCGATGCCCT	960
DB	901	CCAGGCTCAAGGCGGCATGCGCGGAGGATCTCGTGTGACCCATGGCGATGCCCT	960
QY	961	GCTTGCAGAAATCATGTTGGAAATATGGCGCTTTTCTGGAATTCATCGACTGTGGCGGC	1020
DB	961	GCTTGCAGAAATCATGTTGGAAATATGGCGCTTTTCTGGAATTCATCGACTGTGGCGGC	1020
QY	1021	TGGGTGTGGCGGACCGCTATCAGGACATAGCTTGGCTACCGCTGATTTGCTGAAGAGC	1080



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QY 3361 CCAGGTTGCGCGCTGCGCAGACCATCTGGAGTTCTGGGAGAGCGTCTTTACAGGCGCTC 3420  
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Db 5461 TCAGAAATAAGGTAGTAAATTTTGGACTCTTTTCGAGCCGCTCCAAAGCGGAGGAGATGAG 5520  
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Db 7981 AGATCAAGTACT 7992

RESULT 8
ABK91243
ID ABK91243 standard; DNA; 10690 BP.
XX AC ABK91243;
XX DT 15-NOV-2002 (first entry)
XX DE Hepatitis C virus vector construct pHCVNeo.17.m1.
XX KW HCV; ss; pHCVNeo.17m2; adaptive mutation; liver failure; cirrhosis;
KW hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
KW internal ribosome entry site; IRES; NS5A; HCV replication; mutant.
XX OS Hepatitis C virus.
OS Encephalomyocarditis virus.
OS Escherichia coli.
OS Enterobacteria phage T7.
OS Synthetic.

FH Key Location/Qualifiers
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FT /*tag= f
FT misc_feature 7992..10690
FT /*tag= g
FT /note= "Plasmid derived sequences"
XX PN WO200259321-A2.

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XX 01-AUG-2002.
PD 16-JAN-2002; 2002WO-BP000526.
XX 23-JAN-2001; 2001US-0263479P.
XX (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
XX De Francesco R, Migliaccio G, Paonessa G;
XX WPI; 2002-599793/64.
XX New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
XX NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
XX ribosome entry site (IRES) region, useful in studying HCV replication and
XX expression.
XX Example 1; Page; 69pp; English.
XX The invention relates to nucleic acid molecules comprising altered HCV
XX NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
XX internal ribosome entry site (IRES) region coding for one or more NS3,
XX NS5A, or EMCV IRES mutations, respectively. The location of the mutations
XX are detailed in the specification. Also included are (1) an expression
XX vector comprising a nucleotide sequence coding for the altered nucleic
XX acids, which is transcriptionally coupled to an exogenous promoter; (2) a
XX recombinant cell human hepatoma cell comprising the altered nucleic acids
XX ; (3) a recombinant cell produced by introducing into a human hepatoma
XX cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
XX replicon enhanced cell or which containing a functional HCV replicon; (5)
XX an HCV replicon enhanced cells made in the method; and (6) measuring the
XX ability of a compound to affect HCV activity. The HCV replicons and HCV
XX replicon enhanced cells are useful in studying HCV replication and
XX expression, and HCV and host cell interactions, producing HCV RNA and
XX proteins, and providing a system for measuring the ability of a compound
XX to modulate one or more HCV activities e.g. to discover drugs which may
XX treat HCV mediated diseases such as liver failure, cirrhosis and
XX hepatocellular carcinoma. The present sequence is an HCV based vector
XX pHCVNeo.17 mutant of the invention. Note: The present sequence is not
XX shown in the specification but was created by the indexer using the HCV
XX vector sequence appearing as ABK91412 and the information in example 1
XX SQ Sequence 10690 BP; 2333 A; 3046 C; 2908 G; 2403 T; 0 U; 0 Other;
Query Match 100.0%; Score 7990.4; DB 6; Length 10690;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCCAGCCCCCGATTGGGGCGGACACTCCACATAGATCACTCCCTGTGAGGAACACTG 60
Db 1 GCCAGCCCCCGATTGGGGCGGACACTCCACATAGATCACTCCCTGTGAGGAACACTG 60
QY 61 TCTTTCAGCAGAAAGCGTCTAGCCATGGGTTAGTATGAGTGTGTCGACGCTCCAGGAC 120
Db 61 TCTTTCAGCAGAAAGCGTCTAGCCATGGGTTAGTATGAGTGTGTCGACGCTCCAGGAC 120
QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTCGGAAACCGGTGAGTACACCGGAATTGCCAG 180
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Db 301 GTGCTTGGAGTGCCCGGGAGGTCTCGTAGACCGGTGACCATGACGACGAATCTTAAC 360

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DB 361 CTCGAAGAAACCAAGGGCGCCATGATTGAACAAGATGGATTGCACGCAAGTTCTC 420  
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DB 421 CGGCCGCTTGGGTGGAGAGGCTATTTCGGCTATGACTGGGCAACAAGCAATTCGGCTGCT 480  
QY 481 CTGATGCGCGCGTGTTCGGCTGTGACGCGAGGGGCGCCGGTCTCTTTTGTCAAGACCG 540  
DB 481 CTGATGCGCGCGTGTTCGGCTGTGACGCGAGGGGCGCCGGTCTCTTTTGTCAAGACCG 540  
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Qy	2821	GCTCTGTCCAGCATCTGGAGAAATCCCTTTTATGGCAAAGCCATCCCCATCGAGACCATC	2880
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Qy	3481	CTGGTAGCATACAGGCTACGGTGTGCGCCAGGGCTCAGGCTCCACCTTCATCTGGGAC	3540
Db	3481	CTGGTAGCATACAGGCTACGGTGTGCGCCAGGGCTCAGGCTCCACCTTCATCTGGGAC	3540
Qy	3541	CAAAATGTGAAGTGTCTCATACGGCTAAAGCTACGCTGCAACGCGCCCAACGCCCTCTGTG	3600
Db	3541	CAAAATGTGAAGTGTCTCATACGGCTAAAGCTACGCTGCAACGCGCCCAACGCCCTCTGTG	3600
Qy	3601	TATAGGCTGGGACCGTTTCAAAACGAGGTTACTACCAACGCGCCCAACGCCCTCTGTG	3660
Db	3601	TATAGGCTGGGACCGTTTCAAAACGAGGTTACTACCAACGCGCCCAACGCCCTCTGTG	3660



Db 6901 AAGCTCCAGGACTGCAGATGCTCGTATGCGGAGACGACCTTGTCTATCTGTGAAGC 6960  
QY 6961 GCGGGGACCCAGAGGAGCGAGCGCTACGGCCCTTCAGGAGGCTATGACTAGATAC 7020  
Db 6961 GCGGGGACCCAGAGGAGCGAGCGCTACGGCCCTTCAGGAGGCTATGACTAGATAC 7020  
QY 7021 TCTGCCCCCCTCGGGACCGCCCAACACCAAGATACGACTTGGAGTGATAACATATGC 7080  
Db 7021 TCTGCCCCCCTCGGGACCGCCCAACACCAAGATACGACTTGGAGTGATAACATATGC 7080  
QY 7081 TCTCTCAATGTGTCACTGCGGACGATGCTCTGGCAAAAGGCTGACTATCTCACCCGT 7140  
Db 7081 TCTCTCAATGTGTCACTGCGGACGATGCTCTGGCAAAAGGCTGACTATCTCACCCGT 7140  
QY 7141 GACCCACACACCCCTTGGCGGGCTGCGTGGAGACAGCTAGACACACTCCAGTCAAT 7200  
Db 7141 GACCCACACACCCCTTGGCGGGCTGCGTGGAGACAGCTAGACACACTCCAGTCAAT 7200  
QY 7201 TCTGCTAGGCAACATCATCATGTATGCGCCACCTTGGGCAAGGATGATCTGTATG 7260  
Db 7201 TCTGCTAGGCAACATCATCATGTATGCGCCACCTTGGGCAAGGATGATCTGTATG 7260  
QY 7261 ACTCATTTCTTCTCCATCTTCTAGCTCAGGAACACTTGAAGAGCCCTAGATTTCTAG 7320  
Db 7261 ACTCATTTCTTCTCCATCTTCTAGCTCAGGAACACTTGAAGAGCCCTAGATTTCTAG 7320  
QY 7321 ATCTAGGGGCTGTACTCCATTTAGCCACTTGTAGCCACTTACCTACCTCAATCAAGACTC 7380  
Db 7321 ATCTAGGGGCTGTACTCCATTTAGCCACTTGTAGCCACTTACCTACCTCAATCAAGACTC 7380  
QY 7381 CATGGCCCTTAGGCAATTTTCACTCCATGTTACTCTCCAGGTGAGATCAATAGGTTGGT 7440  
Db 7381 CATGGCCCTTAGGCAATTTTCACTCCATGTTACTCTCCAGGTGAGATCAATAGGTTGGT 7440  
QY 7441 TCATGCCCTCAGAAACTTGGGGTACCGCCCTTGGAGTCTGGAGACATCGGSCCAGAACT 7500  
Db 7441 TCATGCCCTCAGAAACTTGGGGTACCGCCCTTGGAGTCTGGAGACATCGGSCCAGAACT 7500  
QY 7501 GTCCGCGTAGGCTACTGTCCAGGGGGGGGGCTGCCACTTGTGGCAAGTACCTCTTC 7560  
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QY 7561 AACTGGGAGTAAGGACCAAGCTCAACTCACTCAATCCCGCTGCGTCCAGTTGGAT 7620  
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QY 7621 TTATCCAGCTGGTTCGTTGCTGTTTACAGCGGGGAGACATATATCACAGCCTGTCTCGT 7680  
Db 7621 TTATCCAGCTGGTTCGTTGCTGTTTACAGCGGGGAGACATATATCACAGCCTGTCTCGT 7680  
QY 7681 GCCCGACCCGCTGGTTCACTGTGCTGCTACTCTTCTGTAGGGTAGGATCTAT 7740  
Db 7681 GCCCGACCCGCTGGTTCACTGTGCTGCTACTCTTCTGTAGGGTAGGATCTAT 7740  
QY 7741 CTACTCCCCAACCGATGAAGGGGAGCTAAACACTCCAGGCCATAGGCCATCTGTTTT 7800  
Db 7741 CTACTCCCCAACCGATGAAGGGGAGCTAAACACTCCAGGCCATAGGCCATCTGTTTT 7800  
QY 7801 TTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860  
Db 7801 TTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860  
QY 7861 TTTTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 7920  
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QY 7921 TAGCTGTGAAGTCCGTGAGCGCTGACTGACGAGAGTCTGATCTGGCTCTCTGTC 7980  
Db 7921 TAGCTGTGAAGTCCGTGAGCGCTGACTGACGAGAGTCTGATCTGGCTCTCTGTC 7980  
QY 7981 AGATCAAGTACT 7992  
Db 7981 AGATCAAGTACT 7992

RESULT 9  
ABK91434  
ID ABK91434 standard; DNA; 10690 BP.  
XX AC ABK91434;  
XX AC  
DT 15-NOV-2002 (first entry)  
XX Hepatitis C virus vector construct pHCVNeo.17m0.  
DE HCV; ss; pHCVNeo.17m2; adaptive mutation; liver failure; cirrhosis;  
XX hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;  
KW internal ribosome entry site; IRES; NS5A; HCV replication; mutant.  
XX Hepatitis C virus.  
OS Encephalomyocarditis virus.  
OS Escherichia coli.  
OS Enterobacteria phage T7.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT 5'UTR 1..341  
FT /tag= a  
FT CDS 342..1181  
FT /tag= b  
FT /product= "Core-neo fusion protein"  
FT misc\_signal 1190..1800  
FT /tag= c  
FT /label= IRES  
FT /note= "Internal ribosome entry site from EMCV"  
FT CDS 1801..7758  
FT /tag= d  
FT /product= "Polyprotein"  
FT /note= "Comprising NS3, NS4A, NS4B, NS5A and NS5B"  
FT mutation replace(5337,C)  
FT /tag= e  
FT 3'UTR 7759..7991  
FT /tag= f  
FT misc\_feature 7992..10690  
FT /tag= g  
FT /note= "Plasmid derived sequences"  
WO200259321-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 16-JAN-2002; 2002WO-EP000526.  
XX  
PR 23-JAN-2001; 2001US-0263479P.  
XX  
PA (RICE-) IST RICERCHIE BIOL MOLECOLARE ANGELETTI.  
XX De Francesco R, Migliaccio G, Paonessa G;  
PI WPI; 2002-599793/64.  
XX  
PT New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV  
PT NS5 encoding region, or encephalomyocarditis virus (EMCV) internal  
PT ribosome entry site (IRES) region, useful in studying HCV replication and  
PT expression.  
XX  
PS Claim 16; Page; 69pp; English.  
XX  
CC The invention relates to nucleic acid molecules comprising altered HCV  
CC NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)  
CC internal ribosome entry site (IRES) region coding for one or more NS3,  
CC NS5A, or EMCV IRES mutations, respectively. The location of the mutations  
CC are detailed in the specification. Also included are (1) an expression  
CC vector comprising a nucleotide sequence coding for the altered nucleic  
CC acids, which is transcriptionally coupled to an exogenous promoter; (2) a  
CC recombinant cell human hepatoma cell comprising the altered nucleic acids

CC ; (3) a recombinant cell produced by introducing into a human hepatoma  
CC cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)  
CC replicon enhanced cell or which containing a functional HCV replicon; (5)  
CC an HCV replicon enhanced cells made in the method; and (6) measuring the  
CC ability of a compound to affect HCV activity. The HCV replicons and HCV  
CC replicon enhanced cells are useful in studying HCV replication and  
CC expression, and HCV and host cell interactions, producing HCV RNA and  
CC proteins, and providing a system for measuring the ability of a compound  
CC to modulate one or more HCV activities e.g. to discover drugs which may  
CC treat HCV mediated diseases such as liver failure, cirrhosis and  
CC hepatocellular carcinoma. The present sequence is an HCV based vector  
CC pHCVneo.17 mutant of the invention. Note: The present sequence is not  
CC shown in the specification but was created by the indexer using the HCV  
CC vector sequence appearing as ABK91412 and the information in Claim 16  
XX  
SQ Sequence 10690 BP; 2335 A; 3044 C; 2908 G; 2403 T; 0 U; 0 Other;  
Query Match 100.0%; Score 7990.4; DB 6; Length 10690;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCCAGCCCCCGATTGGGGCGACATCCACCATAGATCACTCCCTGTGAGGAACACTG 60  
DB 1 GCCAGCCCCCGATTGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAACACTG 60  
QY 61 TCTTCAGCGAGAAGCGTCTAGCCATGGCGTTAGTATGAGTGTGTCGACGCTCCAGGAC 120  
DB 61 TCTTCAGCGAGAAGCGTCTAGCCATGGCGTTAGTATGAGTGTGTCGACGCTCCAGGAC 120  
QY 121 CCCCCTCCCGGAGAGCCATAGTGGTCTCGGAAACCGGTGAGTACACCGGAATTCGCAG 180  
DB 121 CCCCCTCCCGGAGAGCCATAGTGGTCTCGGAAACCGGTGAGTACACCGGAATTCGCAG 180  
QY 181 GAGACCGGGTCCCTTTCTTGATCAACCCGCTCAATGCTGAGATTTGGCGTGCCTCC 240  
DB 181 GAGACCGGGTCCCTTTCTTGATCAACCCGCTCAATGCTGAGATTTGGCGTGCCTCC 240  
QY 241 GCGAGACTGTAGCCGATGATGTGGTTCGGAAGCCCTTGTGTACTGCTGTATAGG 300  
DB 241 GCGAGACTGTAGCCGATGATGTGGTTCGGAAGCCCTTGTGTACTGCTGTATAGG 300  
QY 301 GTGCTTGGAGTGCCTCCCGGAGGTCTCGTAGACCGTGCACCATGACGACGAACTTAAC 360  
DB 301 GTGCTTGGAGTGCCTCCCGGAGGTCTCGTAGACCGTGCACCATGACGACGAACTTAAC 360  
QY 361 CTCAAAGAAAAACCAAAGGGCGCGCCATGATGAAACAGATGATGCAACGAGTCTC 420  
DB 361 CTCAAAGAAAAACCAAAGGGCGCGCCATGATGAAACAGATGATGCAACGAGTCTC 420  
QY 421 CGGCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCAACAGACATCGGCTGCT 480  
DB 421 CGGCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCAACAGACATCGGCTGCT 480  
QY 481 CTGATCGCGCTGTTCGGCTGTTCAGCGAGGGCGCCCGGTTCTTTTGTCAAGACCG 540  
DB 481 CTGATCGCGCTGTTCGGCTGTTCAGCGAGGGCGCCCGGTTCTTTTGTCAAGACCG 540  
QY 541 ACCTGTCCGGTGCCTGAATGAATTCGAGGACGAGCGCGCTATCGTGGCTGGCA 600  
DB 541 ACCTGTCCGGTGCCTGAATGAATTCGAGGACGAGCGCGCTATCGTGGCTGGCA 600  
QY 601 CGACGGGCTTCTTTGGCAGCTGTGCTGAGCTGTGCTCACTGAAGCGGAGGACTGCG 660  
DB 601 CGACGGGCTTCTTTGGCAGCTGTGCTGAGCTGTGCTCACTGAAGCGGAGGACTGCG 660  
QY 661 TCGCTATTGGCGAAGTGCAGGGCGAGGATCTCCTGTCACTCACTCACTGCTCGCGAGA 720  
DB 661 TCGCTATTGGCGAAGTGCAGGGCGAGGATCTCCTGTCACTCACTCACTGCTCGCGAGA 720  
QY 721 AAGTATCCATCATGCTGATGCAATGCGGGGCTGATACGCTTGTATCCGGCTACCTGCC 780  
DB 721 AAGTATCCATCATGCTGATGCAATGCGGGGCTGATACGCTTGTATCCGGCTACCTGCC 780

QY 781 CATTCGACCAACAGCGAAACATCGCATCGAGCGAGCAGTACTCGATGGAAGCGGTC 840  
DB 781 CATTCGACCAACAGCGAAACATCGCATCGAGCGAGCAGTACTCGATGGAAGCGGTC 840  
QY 841 TTGTGATCAGGATCATCTGGACGAGAGCATCAGGGGTCTCGCGCAGCCGAACCTGTCG 900  
DB 841 TTGTGATCAGGATCATCTGGACGAGAGCATCAGGGGTCTCGCGCAGCCGAACCTGTCG 900  
QY 901 CCAGGCTCAAGCGCGCATGTCGCCGAGAGATCTGTCGTGACCCATGCGATGCGCT 960  
DB 901 CCAGGCTCAAGCGCGCATGTCGCCGAGAGATCTGTCGTGACCCATGCGATGCGCT 960  
QY 961 GCTTGGCGAATATCATGTTGGAATGCGCGCTTTTCTCGATTCACTGACTGTGGCGCGC 1020  
DB 961 GCTTGGCGAATATCATGTTGGAATGCGCGCTTTTCTCGATTCACTGACTGTGGCGCGC 1020  
QY 1021 TGGGTGTGGCGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATGCTGAAGAGC 1080  
DB 1021 TGGGTGTGGCGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATGCTGAAGAGC 1080  
QY 1081 TTGGCGGCGAATGGGCTGACCGCTTCTTGAAGAGTCTTCTGAGTTTAAACAGACCAACG 1140  
DB 1081 TTGGCGGCGAATGGGCTGACCGCTTCTTGAAGAGTCTTCTGAGTTTAAACAGACCAACG 1140  
QY 1141 AGCGCATGCGCTTCTATCGCTTCTTGAAGAGTCTTCTGAGTTTAAACAGACCAACG 1200  
DB 1141 AGCGCATGCGCTTCTATCGCTTCTTGAAGAGTCTTCTGAGTTTAAACAGACCAACG 1200  
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DB 1321 CCGTCTTTTGGCAATGAGGGCCCGGAAACCTTGGCGCTTCTCTTCTTGAAGAGCATTCCT 1380  
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DB 1381 AGGGGTCTTTCCTCTCGCAAGGAATGCAAGGTCTGTGATGTTGTTGAAGAGCA 1440  
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1861 AGCTTACAGCGCGGACAGGAACAGGTGTCAGGGGAGGTCCAAAGTGGTCTCCACCGCA 1920  
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2881 AAGGGGGAGGACCTCACTTTCTGCCATTCGAAGAAATGTGATGAGCTCGCGCG 2940  
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QY	4081	GGATAGCATCACTGATGGCAATTCACAGCTCTATCACCAGCCGCTCACACCCAAAT	4140	QY	5161	ACATTCCTGGTGGGCTCAATCAATACCTGGTGGGTACAGCTCCCATCGAGCCGAA	5220
DB	4081	GGATAGCATCACTGATGGCAATTCACAGCTCTATCACCAGCCGCTCACACCCAAAT	4140	DB	5161	ACATTCCTGGTGGGCTCAATCAATACCTGGTGGGTACAGCTCCCATCGAGCCGAA	5220
QY	4141	ACCTTCCTGTTTAAATCTCTGGGGGATGGGTGGCGCCAACTTGTCTCTCCAGCGCT	4200	QY	5221	CGGAGGTAGCAGTCTCACTTCCATGTCTACCGACCCCTCCCAATACCGCGAGAGC	5280
DB	4141	ACCTTCCTGTTTAAATCTCTGGGGGATGGGTGGCGCCAACTTGTCTCTCCAGCGCT	4200	DB	5221	CGGAGGTAGCAGTCTCACTTCCATGTCTACCGACCCCTCCCAATACCGCGAGAGC	5280
QY	4201	GCTTCTGCTTTTGGTAGCGCCGCGATCGCTGGAGCGGTGTGGAGCATAGGCTTGG	4260	QY	5281	GCTAAGCGTAGGCTGGCCAGGGATCTCCCTCCCTCTTGGCCAGCTCATCAGTAGCAG	5340
DB	4201	GCTTCTGCTTTTGGTAGCGCCGCGATCGCTGGAGCGGTGTGGAGCATAGGCTTGG	4260	DB	5281	GCTAAGCGTAGGCTGGCCAGGGATCTCCCTCCCTCTTGGCCAGCTCATCAGTAGCAG	5340
QY	4261	AAGGTGCTGTGATATTTTGGCAGGTATGAGCAGGGGTGCGAGCGGTCTGTGGCC	4320	QY	5341	CTGTCTGCGCTTCTTGAAGCAACATGCACTACCCGTCATGCTCCCGGACGTGAC	5400
DB	4261	AAGGTGCTGTGATATTTTGGCAGGTATGAGCAGGGGTGCGAGCGGTCTGTGGCC	4320	DB	5341	CTGTCTGCGCTTCTTGAAGCAACATGCACTACCCGTCATGCTCCCGGACGTGAC	5400
QY	4321	TTTAAAGTATGAGCGCGAGATGCCCTCCACGAGGACTGGTTAACTACTCTCCCTGCT	4380	QY	5401	CTCATCGAGCCAACTCTCTGTGGCGGAGAGATGGGCGGGAACATCAACCGCGTGGAG	5460
DB	4321	TTTAAAGTATGAGCGCGAGATGCCCTCCACGAGGACTGGTTAACTACTCTCCCTGCT	4380	DB	5401	CTCATCGAGCCAACTCTCTGTGGCGGAGAGATGGGCGGGAACATCAACCGCGTGGAG	5460
QY	4381	ATCCTCTCCCTGGCGCCCTAGTCTGGGTCTGTGGCGACGATATCTGCTGGCAC	4440	QY	5461	TCAGAAAATAAGGTAGTAAATTTTGGACTCTTTTCGAGCGCTCCAAGCGGAGGATGAG	5520
DB	4381	ATCCTCTCCCTGGCGCCCTAGTCTGGGTCTGTGGCGACGATATCTGCTGGCAC	4440	DB	5461	TCAGAAAATAAGGTAGTAAATTTTGGACTCTTTTCGAGCGCTCCAAGCGGAGGATGAG	5520
QY	4441	GTGGGCCAGGGAGGGGGTGTGCAGTGAATGAAACGGCTGATAGCGTTTGGCTTGGCGG	4500	QY	5521	AGGAAAGTATCCTTCCGGCGGAGATCCTCGGAGGTTCAGGAAATTTCCCTCGAGCGATG	5580
DB	4441	GTGGGCCAGGGAGGGGGTGTGCAGTGAATGAAACGGCTGATAGCGTTTGGCTTGGCGG	4500	DB	5521	AGGAAAGTATCCTTCCGGCGGAGATCCTCGGAGGTTCAGGAAATTTCCCTCGAGCGATG	5580
QY	4501	GSTAAACACGCTCCCCACGCACTATGTGCTGAGAGCAGCTGCGAGCACGTGTCACT	4560	QY	5581	CCCATATGGCAGCGCCGATTAACACCTTCCACTGTTAGAGTCTTGAGAGGACCCGAC	5640
DB	4501	GSTAAACACGCTCCCCACGCACTATGTGCTGAGAGCAGCTGCGAGCACGTGTCACT	4560	DB	5581	CCCATATGGCAGCGCCGATTAACACCTTCCACTGTTAGAGTCTTGAGAGGACCCGAC	5640
QY	4561	CAGATCCTCTAGTCTTACCATCACTCAGTCTGAGAGGCTTCCACAGTGGATCAAC	4620	QY	5641	TAGTCTCCTCCAGTGTGTACACGGGTGTCTTGGCGCTTCCAGGCCCCCTCCGATACCA	5700
DB	4561	CAGATCCTCTAGTCTTACCATCACTCAGTCTGAGAGGCTTCCACAGTGGATCAAC	4620	DB	5641	TAGTCTCCTCCAGTGTGTACACGGGTGTCTTGGCGCTTCCAGGCCCCCTCCGATACCA	5700
QY	4621	GAGACTGTCCAGCCATGCTCGGCTCTGGCTTACAGATGTTTGGATGATATGC	4680	QY	5701	CCTCCAGGAGGAGGAGCGGTGTCTCTGCTAGAACTTACCGGTGTCTTCTGCTTGGCG	5760
DB	4621	GAGACTGTCCAGCCATGCTCGGCTCTGGCTTACAGATGTTTGGATGATATGC	4680	DB	5701	CCTCCAGGAGGAGGAGCGGTGTCTCTGCTAGAACTTACCGGTGTCTTCTGCTTGGCG	5760
QY	4681	ACGGTGTGACTGATTTCAAGACCTGCTCCAGTCCAGCTCTCTGCGCGGATTCGCGGA	4740	QY	5761	GAGCTCCCAACAGAGCTTCCGAGCTCCGAAATCTGTCGGCGGTCTGACAGCGGCA	5820
DB	4681	ACGGTGTGACTGATTTCAAGACCTGCTCCAGTCCAGCTCTCTGCGCGGATTCGCGGA	4740	DB	5761	GAGCTCCCAACAGAGCTTCCGAGCTCCGAAATCTGTCGGCGGTCTGACAGCGGCA	5820
QY	4741	GTCCCTCTTCTCATGTCAACGTGGGTACAAGGAGTCTGGCGGGGACGGCATCATG	4800	QY	5821	ACGCGCTCTCTGTGACAGCCCTCCGACGACGCGCGGATCCCGATCTCAGCGAGGGTCTTGG	5880
DB	4741	GTCCCTCTTCTCATGTCAACGTGGGTACAAGGAGTCTGGCGGGGACGGCATCATG	4800	DB	5821	ACGCGCTCTCTGTGACAGCCCTCCGACGACGCGCGGATCCCGATCTCAGCGAGGGTCTTGG	5880
QY	4801	CAAAACACCTGCTGAGGACAGATCACCGGACATGTGAAAACGGTTTCCATGAGG	4860	QY	5881	TCCTCCATGCCCCCTTGGAGGAGCGCGGGATCCCGATCTCAGCGAGGGTCTTGG	5940
DB	4801	CAAAACACCTGCTGAGGACAGATCACCGGACATGTGAAAACGGTTTCCATGAGG	4860	DB	5881	TCCTCCATGCCCCCTTGGAGGAGCGCGGGATCCCGATCTCAGCGAGGGTCTTGG	5940
QY	4861	ATCGTGGGCTTAGGACCTGTAGTAAACAGTGGCATGGAACATTTCCCATTAACCGTAC	4920	QY	5941	TCTACCGTAAAGGAGGCTAGTGAGGACGTCTGTCTCTGCTCGATGCTTACACATGG	6000
DB	4861	ATCGTGGGCTTAGGACCTGTAGTAAACAGTGGCATGGAACATTTCCCATTAACCGTAC	4920	DB	5941	TCTACCGTAAAGGAGGCTAGTGAGGACGTCTGTCTCTGCTCGATGCTTACACATGG	6000
QY	4921	ACCAGCGGCTGCAACGCTTCCCGGGCGCAATTTATCTAGGCGCTGTGGCGGGT	4980	QY	6001	ACAGCGCTTGTATCAOCCCATGCGCTCGGAGGAAACCAAGCTGCCCATCAATGCACTG	6060
DB	4921	ACCAGCGGCTGCAACGCTTCCCGGGCGCAATTTATCTAGGCGCTGTGGCGGGT	4980	DB	6001	ACAGCGCTTGTATCAOCCCATGCGCTCGGAGGAAACCAAGCTGCCCATCAATGCACTG	6060
QY	4981	GCTGTGAGGAGTACGTGAGGTACGCGGGTGGGGATTTCCATCACTGACGGCATG	5040	QY	6061	AGCAACTCTTGTCTCCGTCCACCACTTGTGTATGTATGCTACAACTCTCGAGCGCAAGC	6120
DB	4981	GCTGTGAGGAGTACGTGAGGTACGCGGGTGGGGATTTCCATCACTGACGGCATG	5040	DB	6061	AGCAACTCTTGTCTCCGTCCACCACTTGTGTATGTATGCTACAACTCTCGAGCGCAAGC	6120
QY	5041	ACCACGTGACAAAGTAAAGTCCCGGTGTCAAGTTCGGGCCCGAAATTTCTCAAGAGTG	5100	QY	6121	CTGCGGCAAGAAAGGTCACTTTGACAGACTGCAAGTCTCTGGAAGCACTACCGGAC	6180
DB	5041	ACCACGTGACAAAGTAAAGTCCCGGTGTCAAGTTCGGGCCCGAAATTTCTCAAGAGTG	5100	DB	6121	CTGCGGCAAGAAAGGTCACTTTGACAGACTGCAAGTCTCTGGAAGCACTACCGGAC	6180
QY	5101	GATGGGCTGGTTCACAGGTACGCTCAGCGTGCACACCTCTCAGGAGGAGGTC	5160	QY	6181	GTGCTCAAGGAGTGAAGCGGCTCCAGTTCAGTAAAGCTTAACTTCTATCCGTGGAG	6240
DB	5101	GATGGGCTGGTTCACAGGTACGCTCAGCGTGCACACCTCTCAGGAGGAGGTC	5160	DB	6181	GTGCTCAAGGAGTGAAGCGGCTCCAGTTCAGTAAAGCTTAACTTCTATCCGTGGAG	6240
				QY	6241	GRAGCCTGTAGCTGACGCGCCCACTTCGCGCCAGATCTAAATTTTGGCTATGCGGCAAG	6300

|||||  
6241 GAAAGCTGTAGCTGACGCCCCACATTCGGCCAGATCTAAATTTGGCTATGGGGCAAG 6300  
QY  
6301 GAGCTCCGGAACTATCCAGCAGGCGGTAAACACATCCGCTCCGCTGGAGGACTTG 6360  
Db  
6301 GAGCTCCGGAACTATCCAGCAGGCGGTAAACACATCCGCTCCGCTGGAGGACTTG 6360  
QY  
6361 CTGGAAAGACATGAGACACAAATGACACCAATCATGGCAAAAATGAGGTTTCTGC 6420  
Db  
6361 CTGGAAAGACATGAGACACAAATGACACCAATCATGGCAAAAATGAGGTTTCTGC 6420  
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6481 GTTCGTGTGTGCGAGAAATGCCCCCTTACGATGTGCTCCACCTCCCTCAGGCCGTG 6540  
Db  
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QY  
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Db  
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|||||

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Db  
7381 CATGGCTTTAGCGCAATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGTTGGCT 7440  
QY  
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Db  
7441 TCATGCTCTCAGAAACTTGGGTACCGCCCTTGGCGAGTCTGAGACATCGGCGCAGAAGT 7500  
QY  
7501 GTCCGCGCTAGGCTACTGTCCAGGGGGGAGGCTGCCACTTGTGGCAAGTACCTCTTC 7560  
Db  
7501 GTCCGCGCTAGGCTACTGTCCAGGGGGGAGGCTGCCACTTGTGGCAAGTACCTCTTC 7560  
QY  
7561 AACTGGGAGTAAAGACCAAGCTCAAACTCACTCCCAATCCCGGCTGCGTCCAGTTGGAT 7620  
Db  
7561 AACTGGGAGTAAAGACCAAGCTCAAACTCACTCCCAATCCCGGCTGCGTCCAGTTGGAT 7620  
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7621 TTATCCAGCTGGTTGCTGCTGTTACAGCGGGGAGACATATATCACAGCCTGTCTCGT 7680  
Db  
7621 TTATCCAGCTGGTTGCTGCTGTTACAGCGGGGAGACATATATCACAGCCTGTCTCGT 7680  
QY  
7681 GCCGACCCCGCTGTTTCATGTGTGCTACTCTCTACTTTCTGTAGGGGTAGGCACTAT 7740  
Db  
7681 GCCGACCCCGCTGTTTCATGTGTGCTACTCTCTACTTTCTGTAGGGGTAGGCACTAT 7740  
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7741 CTACTCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTTT 7800  
Db  
7741 CTACTCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTTT 7800  
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7801 TTTCCCTTT 7860  
Db  
7801 TTTCCCTTT 7860  
QY  
7861 TTTTCTCTTTTTTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 7920  
Db  
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QY  
7921 TAGCTGTGAAGGTCCGTGAGCGCTTGAAGTGCAGAGAGTCTGATCTACTGCGCTCTCTGC 7980  
Db  
7921 TAGCTGTGAAGGTCCGTGAGCGCTTGAAGTGCAGAGAGTCTGATCTACTGCGCTCTCTGC 7980  
QY  
7981 AGATCAAGTACT 7992  
Db  
7981 AGATCAAGTACT 7992

## RESULT 10

ADP86264

ID ADP86264 standard; DNA; 11313 BP.

AC ADP86264;

XX AC

XX 23-SEP-2004 (first entry)

XX 23-SEP-2004 (first entry)

DE Hepatitis C virus Con-1 replicon I377/NS-3', plasmid DNA.

XX Hepatitis C virus; HCV; anti-HCV agent; HCV infection; therapy; plasmid; ds.

XX Hepatitis C virus.

XX WO2004055216-A2.

XX 01-JUL-2004.

XX 12-DEC-2003; 2003WO-US039722.

XX 13-DEC-2002; 2002US-0433303P.

XX (FOXC-) FOX CHASE CANCER CENT.

XX Zhu Q, Guo J, Seeger C;

PI

XX WPI; 2004-488079/46.  
DR GENBANK; AJ242652.  
XX  
XX  
PT New cell-line that replicates hepatitis C virus (HCV), where the cell  
line is selected from a non-human cell line and a human non-hepatic cell  
PT line, useful for identifying anti-HCV agents for treating HCV infections.  
XX  
XX Example III; SEQ ID NO 1; 130pp; English.  
XX  
XX The present invention provides hepatitis C virus (HCV) replication cells  
CC and cell lines derived from human non-hepatic cells or non-human cells.  
CC The invention is useful for identifying anti-HCV agents for treating HCV  
CC infections. The present sequence is hepatitis C virus Con-1 replicon  
CC I377/NS3-3' plasmid DNA.  
XX  
XX Sequence 11313 BP; 2347 A; 3334 C; 3152 G; 2480 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 7990.4; DB 12; Length 11313;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCCAGCCCCCGATTGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGAACTACTG 60  
Db 1 GCCAGCCCCCGATTGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGAACTACTG 60  
QY 61 TCTTACGAGAAAGCGTCTAGCCATGGCGTTAGTATGATGATGTCGTCAGCCCTCCAGGAC 120  
Db 61 TCTTACGAGAAAGCGTCTAGCCATGGCGTTAGTATGATGATGTCGTCAGCCCTCCAGGAC 120  
QY 121 CCCCCTCCCGGAGAGCCATAGTGTCTGCGAAACCGGTGAGTACACCGGAATTCGCGAG 180  
Db 121 CCCCCTCCCGGAGAGCCATAGTGTCTGCGAAACCGGTGAGTACACCGGAATTCGCGAG 180  
QY 181 GAGACCGGCTCTTTCTTGATCAACCCGCTCAATGCTGAGATTTGGCGTGGCCCC 240  
Db 181 GAGACCGGCTCTTTCTTGATCAACCCGCTCAATGCTGAGATTTGGCGTGGCCCC 240  
QY 241 GCGAGACTGTAGCGAGTGTGTGGTTCGCGAAAGCGCTGTGCTGACTGCTGATAGG 300  
Db 241 GCGAGACTGTAGCGAGTGTGTGGTTCGCGAAAGCGCTGTGCTGACTGCTGATAGG 300  
QY 301 GTGCTTCGAGTGTGCGGAGGCTCTGTAGACCGTGCACCATGAGCAAGATCTTAAC 360  
Db 301 GTGCTTCGAGTGTGCGGAGGCTCTGTAGACCGTGCACCATGAGCAAGATCTTAAC 360  
QY 361 CTCAAGAAACCAAAAGGCGCGCCATGATTTGAAACAGATGGATTCACGCGAGTTCTC 420  
Db 361 CTCAAGAAACCAAAAGGCGCGCCATGATTTGAAACAGATGGATTCACGCGAGTTCTC 420  
QY 421 CCGCGCTTGGTGGAGGCTATTTCGGCTATGACTGGGACACAGACAAATCGCTGCT 480  
Db 421 CCGCGCTTGGTGGAGGCTATTTCGGCTATGACTGGGACACAGACAAATCGCTGCT 480  
QY 481 CTGATGCGCGCTGTTCGGCTGTTCAGCGAGGCGCGCGCTTTTGTCTAAGACCG 540  
Db 481 CTGATGCGCGCTGTTCGGCTGTTCAGCGAGGCGCGCGCTTTTGTCTAAGACCG 540  
QY 541 ACCTGTCCGCTGCTGATGAATGAACTGCAAGGAGGCGCGCTATCGTGGCTGGCCA 600  
Db 541 ACCTGTCCGCTGCTGATGAATGAACTGCAAGGAGGCGCGCTATCGTGGCTGGCCA 600  
QY 601 CGACGGGCTTCTTGGCGAGCTGTGCTGAGCTGTGCTGAGCGGGAAGGAGTGGC 660  
Db 601 CGACGGGCTTCTTGGCGAGCTGTGCTGAGCTGTGCTGAGCGGGAAGGAGTGGC 660  
QY 661 TGCTATTGGCGAAGTGTGGGCGGAGGATCTCTGTCACTCACTTGTCTGCTGCGGAGA 720  
Db 661 TGCTATTGGCGAAGTGTGGGCGGAGGATCTCTGTCACTCACTTGTCTGCTGCGGAGA 720  
QY 721 AAGTATCATATGCTGATGCAATGCGCGGCTGCATACGCTTGCATCGGCTACTGCC 780  
Db 721 AAGTATCATATGCTGATGCAATGCGCGGCTGCATACGCTTGCATCGGCTACTGCC 780

QY 781 CATTGACCAACCAAGCGAATCGATCGATCGAGCGACGCTACTCGATGGAAGCGGTC 840  
Db 781 CATTGACCAACCAAGCGAATCGATCGATCGAGCGACGCTACTCGATGGAAGCGGTC 840  
QY 841 TTGTGATTCAGATGATCTGACGAAGAGCATCAGGGGCTCGCGCCAGCGAATGTTTCG 900  
Db 841 TTGTGATTCAGATGATCTGACGAAGAGCATCAGGGGCTCGCGCCAGCGAATGTTTCG 900  
QY 901 CCAGGCTCAAGCGCGCATGCGCGAGGATCTCGTGTGACCATGCGGATGCT 960  
Db 901 CCAGGCTCAAGCGCGCATGCGCGAGGATCTCGTGTGACCATGCGGATGCT 960  
QY 961 GCTTCCGGAATATCATGTTGGAATGCGCGCTTTCTGGATTCATGCACTGTGCGCGC 1020  
Db 961 GCTTCCGGAATATCATGTTGGAATGCGCGCTTTCTGGATTCATGCACTGTGCGCGC 1020  
QY 1021 TGGGTGTGCGGACCGCTATCAGGACATAGCGTTGGCTACCGCTGATATTGCTGAAGAGC 1080  
Db 1021 TGGGTGTGCGGACCGCTATCAGGACATAGCGTTGGCTACCGCTGATATTGCTGAAGAGC 1080  
QY 1081 TTGGGCGGAATGGGCTGACCGCTTCTGCTGCTTTACGCTATCGCGCTCCCGATTCGC 1140  
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QY 1141 AGCGATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCAACAGC 1200  
Db 1141 AGCGATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCAACAGC 1200  
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAACTGCTGGC 1260  
Db 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAACTGCTGGC 1260  
QY 1261 CGAAGCGCTTGAATTAAGCGCGTGTGCTATATGTTTATTTTCCACATATG 1320  
Db 1261 CGAAGCGCTTGAATTAAGCGCGTGTGCTATATGTTTATTTTCCACATATG 1320  
QY 1321 CCGTCTTTTGGCAATGTGAGGCGCGGAAACCTGCGCCCTCTCTTCTTGAAGAGATTCCT 1380  
Db 1321 CCGTCTTTTGGCAATGTGAGGCGCGGAAACCTGCGCCCTCTCTTCTTGAAGAGATTCCT 1380  
QY 1381 AGGGGTCTTTCCTCTCGCCAAAGGAATGCAAGGCTGTGTAATGCTGTAAGAGAGCA 1440  
Db 1381 AGGGGTCTTTCCTCTCGCCAAAGGAATGCAAGGCTGTGTAATGCTGTAAGAGAGCA 1440  
QY 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACAAACGCTGTGAGCGACCTTTGAGCGAGCGG 1500  
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QY 1501 AACCCCGACCTGGCGACAGTGCCTCTGCGGCCAAAGCCACGCTGTAAGATACACCT 1560  
Db 1501 AACCCCGACCTGGCGACAGTGCCTCTGCGGCCAAAGCCACGCTGTAAGATACACCT 1560  
QY 1561 GCAAAGCGGCAACAAACCGAGTGCACGTTGTGAGTTGGATGTTGGAAAGAGTCAAA 1620  
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QY 1621 TGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGGATGCCAGAGGATACCCATGCT 1680  
Db 1621 TGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGGATGCCAGAGGATACCCATGCT 1680  
QY 1681 ATGGATCTGATCTGGGCGCTCGGTGCACATGCTTTTACATGTTTGTAGTCGAGGTTAAA 1740  
Db 1681 ATGGATCTGATCTGGGCGCTCGGTGCACATGCTTTTACATGTTTGTAGTCGAGGTTAAA 1740  
QY 1741 AACGCTCTAGGCGCCCGAACCAACCGGGGAGCTGGTTCCTTTGAAAAACAGATATACC 1800  
Db 1741 AACGCTCTAGGCGCCCGAACCAACCGGGGAGCTGGTTCCTTTGAAAAACAGATATACC 1800  
QY 1801 ATGGCGCTATTAAGCGCTACTCCCAAGAGCGGAGGCTACTTTGGTGTGATCATCACT 1860  
Db 1801 ATGGCGCTATTAAGCGCTACTCCCAAGAGCGGAGGCTACTTTGGTGTGATCATCACT 1860



Db 4021 TGGAAATTCATCAGCGGATACAAATATTTAGAGGCTTGTCCACTCTGCTCGCAACCCC 4080  
Qy 4081 GCGATAGCATCACTGATGGCAATTCACAGCCTCTATCACCAGCGGCTCACACCAACAT 4140  
Db 4081 GCGATAGCATCACTGATGGCAATTCACAGCCTCTATCACCAGCGGCTCACACCAACAT 4140  
Qy 4141 ACCCTCTGTTTAAATCATCTGAGGGGATGGGTGGCGGCCCAACTTGTCTCTCCACGCGCT 4200  
Db 4141 ACCCTCTGTTTAAATCATCTGAGGGGATGGGTGGCGGCCCAACTTGTCTCTCCACGCGCT 4200  
Qy 4201 GCTTCTGCTTTCGTAGGCGCGGCATCGCTGGAGCGGCTGTGGCAGCATAGGCTTGGG 4260  
Db 4201 GCTTCTGCTTTCGTAGGCGCGGCATCGCTGGAGCGGCTGTGGCAGCATAGGCTTGGG 4260  
Qy 4261 AAGTGTCTTGTGATATTTTGGCAGGTTATGGAGCAGGGTGGCAGCGCTTGGG 4320  
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Qy 4321 TTAAAGGTATCAGCGGCGAGATGCCCTCCACGAGGACCTGGTTAAACCTACTCCCTGCT 4380  
Db 4321 TTAAAGGTATCAGCGGCGAGATGCCCTCCACGAGGACCTGGTTAAACCTACTCCCTGCT 4380  
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Qy 4501 GGTAAACAGCTCTCCCGCAGCACTATGTGCTGAGAGGACGCTCGCAGCACGTGTCACT 4560  
Db 4501 GGTAAACAGCTCTCCCGCAGCACTATGTGCTGAGAGGACGCTCGCAGCACGTGTCACT 4560  
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Qy 4621 GAGGACTGTCTCAGCGCATGCTCCGCTCGTGTCTAGAGATGTTTGGGATTCGATATGC 4680  
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Qy 4681 ACCGTGTGACTTCAAGACTGTGCTCCAGTCCAGTCTCTGCGCGGATTTGCCGGGA 4740  
Db 4681 ACCGTGTGACTTCAAGACTGTGCTCCAGTCCAGTCTCTGCGCGGATTTGCCGGGA 4740  
Qy 4741 GTCCCTCTCTCTCATCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 4800  
Db 4741 GTCCCTCTCTCTCATCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 4800  
Qy 4801 CAAACCACTGCGCATGTGGAGCACAGATCACCGGACATGTGAAAACGGTTCCATGAGG 4860  
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Qy 4861 ATGTGGGGCTTAGGACTGTAGTAAACAGTGGCATGGAACATTTCCCAATTAACGCTAC 4920  
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Db 5041 ACCACTGACAACTGAAAGTCCCTGTGTCAGGTTCCGGCCCCCGAAATTTCTTCAAGAGTG 5100  
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Qy 5161 ACATTCTGTGTCGGGCTCAATCAATACCTGTGGTTCAGAGTCCCATGCGAGCCGAA 5220  
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QY |  
QY 7981 AGATCAAGTACT 7992  
Db |  
QY 7981 AGATCAAGTACT 7992

## RESULT 11

AAA98968  
ID AAA98968 standard; DNA; 7989 BP.  
XX  
AC AAA98968;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Hepatitis C virus DNA fragment SEQ ID NO: 4.  
XX  
KW Cell culture; therapy; infection; vaccine; diagnosis; gene therapy; ds.  
XX  
OS Hepatitis C virus.  
XX  
PN DE19915178-Al.  
XX  
PD 05-OCT-2000.  
XX  
PF 03-APR-1999; 99DE-01015178.  
XX  
PR 03-APR-1999; 99DE-01015178.  
XX  
PA (UYMA-) UNIV MAINZ GUTENBERG JOHANNES.  
XX  
PI Bartenschlager R;

XX WPI; 2000-629140/61.  
XX Cell culture system for hepatitis C virus, useful e.g. in screening for  
PT therapeutic agents, comprises human hepatoma cells containing a viral RNA  
PT construct that includes a selectable gene.  
XX Claim 8; Page 37-43; 58pp; German.  
XX This invention describes a novel Hepatitis C virus (HCV) cell culture  
CC system comprising human hepatoma cells that contain an integrated HCV-RNA  
CC construct (I). (I) contains the HCV-specific RNA segments 5'-NTR (non-  
CC translated region), NS (non-structural), NS4A, NS4B, NS5A, NS5B and 3'-  
CC NTR, and a selectable (marker) gene (II). The cell cultures, and/or (I),  
CC are used to prepare, evaluate and/or test therapeutic and/or diagnostic  
CC agents for HCV infections, and to prepare vaccines against HCV infection  
CC (particularly preparation of attenuated HCV). The can also be used for  
CC preparation of a liver-specific delivery system for gene therapy, and to  
CC identify cells permissive for HCV replication. Virus RNA replicates  
CC autonomously and with high efficiency in this cellular system, so that  
CC variations in replication rates can be measured (for screening antiviral  
CC agents) quantitatively or qualitatively, using standard laboratory  
CC equipment. Efficient replication of HCV RNA is only achieved when the  
CC specified RNA segments are present and when the transfected cells are  
CC maintained under permanent selection pressure  
XX  
XX Sequence 7989 BP; 1647 A; 2368 C; 2243 G; 1731 T; 0 U; 0 Other;  
Query Match 100.0%; Score 7989; DB 3; Length 7989;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 7989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCCAGCCCCCGATTGGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAACACTG 60  
DB 1 GCCAGCCCCCGATTGGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAACACTG 60  
QY 61 TCTTCAGCAGAAACCGTCTAGCATAGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 120  
DB 61 TCTTCAGCAGAAACCGTCTAGCATAGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 120  
QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGAACCGGTGAGTGTGAGTGTGAGTGTGAGTGTG 180  
DB 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGAACCGGTGAGTGTGAGTGTGAGTGTGAGTGTG 180  
QY 181 GACGACCGGGTCTTCTTGTGATCAACCGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 240  
DB 181 GACGACCGGGTCTTCTTGTGATCAACCGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 240  
QY 241 GCGAGACTGCTAGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 300  
DB 241 GCGAGACTGCTAGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 300  
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DB 301 GTGCTTGGAGTGTGCGGAGGTCTCGTAGACCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 360  
QY 361 CTCAGAGAAAACCAAGGGCGCGCCATGATTGAACAGATGATGATGATGATGATGATGATGATGATG 420  
DB 361 CTCAGAGAAAACCAAGGGCGCGCCATGATTGAACAGATGATGATGATGATGATGATGATGATGATG 420  
QY 421 CGGCGCTTGGTGGAGAGGTATTTCGGTATGATGATGATGATGATGATGATGATGATGATGATGATG 480  
DB 421 CGGCGCTTGGTGGAGAGGTATTTCGGTATGATGATGATGATGATGATGATGATGATGATGATGATG 480  
QY 481 CTGATGCGCGCTGTTTCGGCTGTACAGCGAGGGCGCCGGTCTTTTGTTCAGACCG 540  
DB 481 CTGATGCGCGCTGTTTCGGCTGTACAGCGAGGGCGCCGGTCTTTTGTTCAGACCG 540  
QY 541 ACTGTCCGGTGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600  
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DB TGCTATTGGCGAAGTGCCTGGGCGAGGATCTCTCTCACTCACTCACTTGTCTCTGCGGAGA 720  
QY AAGTATCCATCATGCTGATGCAATGCGGCGCTGATACGCTTGTATCGGCTACTCTGCTGC 780  
DB AAGTATCCATCATGCTGATGCAATGCGGCGCTGATACGCTTGTATCGGCTACTCTGCTGC 780  
QY CATTCGACCAACCAAGCGAATCATCGATCGAGGAGCATCTGCTGAGTGTGAGTGTGAGTGTG 840  
DB CATTCGACCAACCAAGCGAATCATCGATCGAGGAGCATCTGCTGAGTGTGAGTGTGAGTGTG 840  
QY TTGTCGATCAGGATGATCGAGGAGCATCAGGAGCATCAGGAGCATCAGGAGCATCAGGAGCAT 900  
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QY CCAGGCTCAAGGCGGCGATGCGGAGGAGCATCTGCTGAGTGTGAGTGTGAGTGTGAGTGTG 960  
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DB TGGCTCTCTCAAGCGTATTCAACAAAGGCGCTGAGGATGCTGAGGATGCTGAGGATGCTGAG 1680  
QY ATGGGATCTGATCTGCGGCGCTGCGTGCACATGCTTTACATGTTGTGTAGTGTGAGGTTAA 1740



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Db	3901	GAACTATTCAACAGAGGCAATCGGTTGCTGCAACAGCCACACAGAGCGAGGCT	3960	QY	5041	ACCACTGACAACTAAAGTGCCTGTGTCAGGTTCCGGCCCCCGAAATTTCTTACAGAGTG	5100
QY	3961	GCTGCTCCGCTGGTGGATCCAGTGGCGGACCTTCGAAGCCTTCTGGCGGAAAGCATATG	4020	Db	5041	ACCACTGACAACTAAAGTGCCTGTGTCAGGTTCCGGCCCCCGAAATTTCTTACAGAGTG	5100
Db	3961	GCTGCTCCGCTGGTGGATCCAGTGGCGGACCTTCGAAGCCTTCTGGCGGAAAGCATATG	4020	QY	5101	GATGGGTGCGGTGTCACAGGTACGCTCCAGCGTGAACCCCTCTACGGGAGGAGGTC	5160
QY	4021	TGGATTTTATCAGCGGGATACAAATATTTAGCAGGCTTGTCCACTCTCTGCTGGGAAACCC	4080	Db	5101	GATGGGTGCGGTGTCACAGGTACGCTCCAGCGTGAACCCCTCTACGGGAGGAGTC	5160
Db	4021	TGGATTTTATCAGCGGGATACAAATATTTAGCAGGCTTGTCCACTCTCTGCTGGGAAACCC	4080	QY	5161	ACATTTCTGCTGGGCTCAATCAATACCTGTTGGTTCACAGCTCCCATCGAGCCCGAA	5220
QY	4081	CGGATAGCATCACTGATGCAATTCACAGCTTCATACAGCGCGCTCACACCCAAAT	4140	Db	5161	ACATTTCTGCTGGGCTCAATCAATACCTGTTGGTTCACAGCTCCCATCGAGCCCGAA	5220
Db	4081	CGGATAGCATCACTGATGCAATTCACAGCTTCATACAGCGCGCTCACACCCAAAT	4140	QY	5221	CCGACGCTAGCAGTGTCTCATTTCCATGTCAACGACCCCTCCACATTTAGGGGGAGAG	5280
QY	4141	ACCTCTCTTTTAACTCTGGGGGATGGGTGGCGCCCACTCTCTCCAGCGCT	4200	Db	5221	CCGACGCTAGCAGTGTCTCATTTCCATGTCAACGACCCCTCCACATTTAGGGGGAGAG	5280
Db	4141	ACCTCTCTTTTAACTCTGGGGGATGGGTGGCGCCCACTCTCTCCAGCGCT	4200	QY	5281	GCTAAGCTAGGCTGGCCAGGGGATCTCCCCCTCTTGGCCAGCTCATCAGTAGCCAG	5340
QY	4201	GCTTCTGCTTTGATAGCGCGGATCGCTGGAGCGGCTGTGGCAGCATAGGCTTGG	4260	Db	5281	GCTAAGCTAGGCTGGCCAGGGGATCTCCCCCTCTTGGCCAGCTCATCAGTAGCCAG	5340
Db	4201	GCTTCTGCTTTGATAGCGCGGATCGCTGGAGCGGCTGTGGCAGCATAGGCTTGG	4260	QY	5341	CTGTCTGCGCTTCTTGAAGCAACATGACCTACCCCTCTTGGCCAGCTCATCAGTAGCCAG	5400
QY	4261	AGGTCCTTGTGATATTTTGGCAGGTTATGGAGCAGGGTGGCAGCGGCTCGTGGCC	4320	Db	5341	CTGTCTGCGCTTCTTGAAGCAACATGACCTACCCCTCTTGGCCAGCTCATCAGTAGCCAG	5400
Db	4261	AGGTCCTTGTGATATTTTGGCAGGTTATGGAGCAGGGTGGCAGCGGCTCGTGGCC	4320	QY	5401	CTCATCGAGGCCAACCTCTCTGGCGGAGAGTGGCGGGAAATCATCCCCGGTGGAG	5460
QY	4321	TTTTAAGGTGATGAGCGGAGATGCTCTCCACCGAGGACCTGGTTAACTTCTCTGCT	4380	Db	5401	CTCATCGAGGCCAACCTCTCTGGCGGAGAGTGGCGGGAAATCATCCCCGGTGGAG	5460
Db	4321	TTTTAAGGTGATGAGCGGAGATGCTCTCCACCGAGGACCTGGTTAACTTCTCTGCT	4380	QY	5461	TCAGAAAAATAGGTAGTAAATTTTGGACTCTTTCGAGCGCTTCCAAAGCGGAGGAGTAG	5520
QY	4381	ATCTCTCTCCCTGGCGGCTAGTGTGCGGGTGTGTGGCAGGATGCTGCTGGCAG	4440	Db	5461	TCAGAAAAATAGGTAGTAAATTTTGGACTCTTTCGAGCGCTTCCAAAGCGGAGGAGTAG	5520
Db	4381	ATCTCTCTCCCTGGCGGCTAGTGTGCGGGTGTGTGGCAGGATGCTGCTGGCAG	4440	QY	5521	AGGGAATATTCCTTTCGCGGAGATCTCTGGGAGGTCAGGAAATTTCCCTCGAGCGATG	5580
QY	4441	GTGGGCCAGGGAGGGGCTGTGCACTGAGTGAACCGGCTGTAGCGTTCGCTTCGGG	4500	Db	5521	AGGGAATATTCCTTTCGCGGAGATCTCTGGGAGGTCAGGAAATTTCCCTCGAGCGATG	5580
Db	4441	GTGGGCCAGGGAGGGGCTGTGCACTGAGTGAACCGGCTGTAGCGTTCGCTTCGGG	4500	QY	5581	CCCATATGGGACGCGCCGGATTAACACCTCTCACTTTAGAGTCTTGGAGGACCCGGAC	5640
QY	4501	GGTAACACGCTCTCCCGACGATATGTGCTGAGAGCGACGCTGCAACAGCTGTCACT	4560	Db	5581	CCCATATGGGACGCGCCGGATTAACACCTCTCACTTTAGAGTCTTGGAGGACCCGGAC	5640
Db	4501	GGTAACACGCTCTCCCGACGATATGTGCTGAGAGCGACGCTGCAACAGCTGTCACT	4560	QY	5641	TACGTCCCTCCAGTGGTACAGGGGTGTCATTCGCGCTGCGGAGGAGGATGAG	5700
QY	4561	CAGATCTCTCTAGTCTTACCATCACTCAGCTGCTGAGAGGCTTCAACAGTGGATCAAC	4620	Db	5641	TACGTCCCTCCAGTGGTACAGGGGTGTCATTCGCGCTGCGGAGGAGGATGAG	5700
Db	4561	CAGATCTCTCTAGTCTTACCATCACTCAGCTGCTGAGAGGCTTCAACAGTGGATCAAC	4620	QY	5701	CCTCCAGGAGGAGAGGAGCGGTTCTCTGTGAGAACTCTACCGTGTCTTCTGCTTGGG	5760
QY	4621	GAGGACTGCTCCAGCGCATGCTCGGCTCGGCTTAAGAGATGTTTGGGATTTGATATGC	4680	Db	5701	CCTCCAGGAGGAGAGGAGCGGTTCTCTGTGAGAACTCTACCGTGTCTTCTGCTTGGG	5760
Db	4621	GAGGACTGCTCCAGCGCATGCTCGGCTCGGCTTAAGAGATGTTTGGGATTTGATATGC	4680	QY	5761	GAGCTCGGCAACAAAGACCTTCGGAGCTCCGAATCGTTCGGCGTGCAGAGCGGACGCA	5820
QY	4681	ACGGTGTGACTGATTTCAAGACCTGGGCTCCAGTCCAAAGCTCCTCCCGGATTCGGGGA	4740	Db	5761	GAGCTCGGCAACAAAGACCTTCGGAGCTCCGAATCGTTCGGCGTGCAGAGCGGACGCA	5820
Db	4681	ACGGTGTGACTGATTTCAAGACCTGGGCTCCAGTCCAAAGCTCCTCCCGGATTCGGGGA	4740	QY	5821	ACGGCTCTCTCTGACAGCGCTTCGAGCGGAGCGGAGATCCCGATCTCAGCGACGGTCTTG	5880
QY	4741	GTCCCTCTTCTCAGTCAAGTGGATCAAGGAGTCTGGCGGGGACGCGCATATG	4800	Db	5821	ACGGCTCTCTCTGACAGCGCTTCGAGCGGAGCGGAGATCCCGATCTCAGCGACGGTCTTG	5880
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QY	4921	ACCAAGGCGCTGAGCGCTCCCGGCGGCAATTTTCTAGGCGGCTGTGCGGGTG	4980	Db	6001	ACAGGGCCCTGATACAGCCATGCGCTGCGGAGGAAACCAAGCTGCCATCAATGCACTG	6060
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Qy 7981 AGATCAAGT 7989  
Db 7981 AGATCAAGT 7989

## RESULT 12

ADJ57845

ID ADJ57845 standard; DNA; 7989 BP.

XX

AC ADJ57845;

XX

DT 06-MAY-2004 (first entry)

XX

DE HCV replicon encoding sequence.

XX

KW hepatitis C virus; HCV; Antiinflammatory; Hepatototropic; Virucide; ds;

XX

OS HCV replicon.

XX

XX Unidentified.

XX

Key Location/Qualifiers  
 CDS 1801..7759  
 /\*tag= a  
 /product= "HCV replicon"  
 WO2004015131-A2.  
 19-FEB-2004.  
 12-AUG-2003; 2003WO-US025260.  
 12-AUG-2002; 2002US-0402661P.  
 (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 Gao M, Lemm JA, O'boyle DR, Nower P, Rigat K, Sun J;  
 WPI; 2004-180685/17.  
 P-PSDB; ADJ57846.  
 Use of hepatitis C virus assays or reporter assays, e.g. identifying a  
 compound that inhibits hepatitis C virus RNA replication or identifying a  
 compound that modulates the activity of a gene of interest.  
 Claim 3; SEQ ID NO 1; 45pp; English.  
 The present invention relates to the use of hepatitis C virus (HCV)  
 assays for identifying a compound that inhibits HCV RNA replication and  
 reporter assays for identifying a compound that modulates the activity of  
 a gene of interest. The assays are useful for identifying a compound that  
 inhibits HCV RNA replication or for identifying a compound that modulates  
 the activity of a gene of interest. The HCV assay is useful for high  
 throughput screening that quantifies both the amount of HCV RNA  
 replication inhibitory activity associated with a test compound and the  
 amount of cytotoxicity associated with the test compound. The compound is  
 useful for treating hepatitis C infection. Assays of the invention have  
 distinct advantages when compared to qRT-PCR or other methods in that  
 assays of the invention may take place in situ in a detergent based crude  
 cell lysate, which requires no further preparation prior to performing  
 the assays. The assays do not also involve numerous manipulations to add  
 or subtract reagents after addition of test compounds and are desirably  
 based on a viral protein which is required by the HCV replicon for  
 replication. The present sequence represents a HCV replicon encoding  
 sequence used in the assay of the invention.  
 Sequence 7989 BP; 1647 A; 2368 C; 2243 G; 1731 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 7989; DB 12; Length 7989;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 7989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCACGCCCGGATGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAACCTACTG 60  
 DB 1 GCACGCCCGGATGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGGAACCTACTG 60  
 QY 61 TCTTCACGAGAAAGCGCTAGCCATGGGCTTAGTATAGTGTGCGAGCCTCCAGGAC 120  
 DB 61 TCTTCACGAGAAAGCGCTAGCCATGGGCTTAGTATAGTGTGCGAGCCTCCAGGAC 120  
 QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAG 180  
 DB 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAG 180  
 QY 181 GACGACCGGGTCTTTCTTGGATCAACCGCTCAATGCTGAGATTTGGGCGTCCCCC 240  
 DB 181 GACGACCGGGTCTTTCTTGGATCAACCGCTCAATGCTGAGATTTGGGCGTCCCCC 240  
 QY 241 GCGAGCTGCTAGCCGAGTAGTGTGGGTGCGGAAGCCTTGTGCTACTGCTGATAGG 300  
 DB 241 GCGAGCTGCTAGCCGAGTAGTGTGGGTGCGGAAGCCTTGTGCTACTGCTGATAGG 300  
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 DB 301 GTGCTTGGAGTGGCCCGGGAGGTCTCGTAGACCGGTGACCATGACGACGAATCCTAAAC 360

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 Db 361 CTCAAAGAAAACCAAGAGGCGCGCATGATTGAACAAGATGGATTGCACGAGTTCTC 420  
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 Db 421 CGGCCGCTTGGGTGGAGAGGCTATTCCGGCTATGACTGGGCAACAACAGCAATCGGCTGCT 480  
 QY 481 CTGATGCGCGCTGTTCCGGCTGTACGCGAGGGGCGCCGGTCTTTTGTCAAGACCG 540  
 Db 481 CTGATGCGCGCTGTTCCGGCTGTACGCGAGGGGCGCCGGTCTTTTGTCAAGACCG 540  
 QY 541 ACCTGTCGGTGCCTGAAATGAATGAACTGAGGAGGCGAGCGCGCTATCGTGGTGGCCA 600  
 Db 541 ACCTGTCGGTGCCTGAAATGAATGAACTGAGGAGGCGAGCGCGCTATCGTGGTGGCCA 600  
 QY 601 CGACGGGCGTTCCTTGCAGAGTGTGCTGCACGTTGTCACTGAAGCGGGAAGGACTGGC 660  
 Db 601 CGACGGGCGTTCCTTGCAGAGTGTGCTGCACGTTGTCACTGAAGCGGGAAGGACTGGC 660  
 QY 661 TGTATTGGGCGAAGTGGCGGCGAGATCTCTGTCATCTCACTTGTCTTCCGAG 720  
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 QY 721 AAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATAGCTTGATCCGGCTACCTGCC 780  
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 QY 841 TTGTGATCAGATGATCTGAGAAAGAGATCAGGGGTTCGCGCAGCGAACTGTTCG 900  
 Db 841 TTGTGATCAGATGATCTGAGAAAGAGATCAGGGGTTCGCGCAGCGAACTGTTCG 900  
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Qy	3661	ATGGCATGATGTCGGTGCACCTGGAGTTCGTACAGAGCACTGGGTGCTGGTAGCGGA	3720	4741	GTCCCTTCTTCTCATGTCAACGTGGGTACAAAGGAGTCTGGGGGGCGACGCAATCATG	4800
Db	3661	ATGGCATGATGTCGGTGCACCTGGAGTTCGTACAGAGCACTGGGTGCTGGTAGCGGA	3720	4741	GTCCCTTCTTCTCATGTCAACGTGGGTACAAAGGAGTCTGGGGGGCGACGCAATCATG	4800
Qy	3721	GTCCATAGACGCTTGGCGGCTATTGCTGACAAACAGGAGCGTGTTCATTGTGGCAGG	3780	4801	CAAAACACCTGCGCCATGTGGAGCAGATCACCGGACATGTGAAAACGGTTCATGAGG	4860
Db	3721	GTCCATAGACGCTTGGCGGCTATTGCTGACAAACAGGAGCGTGTTCATTGTGGCAGG	3780	4801	CAAAACACCTGCGCCATGTGGAGCAGATCACCGGACATGTGAAAACGGTTCATGAGG	4860
Qy	3781	ATCATCTTGTCCGAAAGCCGGCATCATTTCCGACAGGAAAGTTCCTTTACCGGAGTTC	3840	4861	ATCGTGGGCTAGGACCTGTACTAACAGTGCATGGAACATTTCCCAATTAACCGCTAC	4920
Db	3781	ATCATCTTGTCCGAAAGCCGGCATCATTTCCGACAGGAAAGTTCCTTTACCGGAGTTC	3840	4861	ATCGTGGGCTAGGACCTGTACTAACAGTGCATGGAACATTTCCCAATTAACCGCTAC	4920
Qy	3841	GATGAGATGAAGAGTGGCTCACACTCCCTTACATCAACAGGAAATGCACTGCC	3900	4921	ACCAAGGGCCCTGACAGCCCTCCCGGGCCCAAAATTAATTTAGGGGCTGTGGCGGGTG	4980
Db	3841	GATGAGATGAAGAGTGGCTCACACTCCCTTACATCAACAGGAAATGCACTGCC	3900	4921	ACCAAGGGCCCTGACAGCCCTCCCGGGCCCAAAATTAATTTAGGGGCTGTGGCGGGTG	4980
Qy	3901	GAACAATTCAAACAGAGGCAATCGGTTGCTGCAACAGCCACCAAGCAAGCGAGGCT	3960	4981	GCTGCTGAGGAGTACGTTGAGGTTACCGGGTGGGGATTTCCACTACGTGACGGCATG	5040
Db	3901	GAACAATTCAAACAGAGGCAATCGGTTGCTGCAACAGCCACCAAGCAAGCGAGGCT	3960	4981	GCTGCTGAGGAGTACGTTGAGGTTACCGGGTGGGGATTTCCACTACGTGACGGCATG	5040
Qy	3961	GCTGCTCCGTTGGTGAATCAAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATG	4020	5041	ACCACTGACAACTGTAAGTGCCTGTCAGGTTCCGGCCCGGAAATTTCTTACAGAAAGTG	5100
Db	3961	GCTGCTCCGTTGGTGAATCAAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATG	4020	5041	ACCACTGACAACTGTAAGTGCCTGTCAGGTTCCGGCCCGGAAATTTCTTACAGAAAGTG	5100
Qy	4021	TGGAATTTTCATCAGCGGATCAATATTTAGAGGTTTGTCCACTGCTGGCAACCCC	4080	5101	GATGGGTGGGTTGACAGGTACGCTCCAGCGTGCAAAACCCCTCTTACGGGAGGATG	5160
Db	4021	TGGAATTTTCATCAGCGGATCAATATTTAGAGGTTTGTCCACTGCTGGCAACCCC	4080	5101	GATGGGTGGGTTGACAGGTACGCTCCAGCGTGCAAAACCCCTCTTACGGGAGGATG	5160
Qy	4081	GGATAGCATCACTGATGGATTCACAGCTCTATCACCAGCCGCTCACCACCAACAT	4140	5161	ACATTCCTGCTGGGCTCAATCAATACCTGTTGGGTCCAGCTCCCATGCGAGCCGAA	5220
Db	4081	GGATAGCATCACTGATGGATTCACAGCTCTATCACCAGCCGCTCACCACCAACAT	4140	5161	ACATTCCTGCTGGGCTCAATCAATACCTGTTGGGTCCAGCTCCCATGCGAGCCGAA	5220
Qy	4141	ACCTCTCTGTTTAAATCCTCGGGGATGGTGGCGGCCCAACTTGTCTTCCAGCGCT	4200	5281	CCGACGTAGCAGTGTCACTTCCATGCTCACCGACCCCTCCACATTTACCGCGGAGACG	5280
Db	4141	ACCTCTCTGTTTAAATCCTCGGGGATGGTGGCGGCCCAACTTGTCTTCCAGCGCT	4200	5281	CCGACGTAGCAGTGTCACTTCCATGCTCACCGACCCCTCCACATTTACCGCGGAGACG	5280
Qy	4201	GCTTCTGCTTTTGGTAGGCGCGGCATCGCTGGAGCGGCTGTTGGCAGCATAGGCTTGG	4260	5341	GCTAAGCGTAGGCTGGCGAGGGATCTCCCGCTCTTGGGCGAGCTATCATAGTAGCCAG	5340
Db	4201	GCTTCTGCTTTTGGTAGGCGCGGCATCGCTGGAGCGGCTGTTGGCAGCATAGGCTTGG	4260	5341	GCTAAGCGTAGGCTGGCGAGGGATCTCCCGCTCTTGGGCGAGCTATCATAGTAGCCAG	5340
Qy	4261	AAGTGTCTTGGATATTTTGGCAGGTTATGGAGCAGGGTGGAGCGCGCTCGTGCC	4320	5401	CTGCTGCGCTTCTTGAAGGCAACATGCACTACCGCTCATGCTCCCGGACCTGAC	5400
Db	4261	AAGTGTCTTGGATATTTTGGCAGGTTATGGAGCAGGGTGGAGCGCGCTCGTGCC	4320	5401	CTGCTGCGCTTCTTGAAGGCAACATGCACTACCGCTCATGCTCCCGGACCTGAC	5400
Qy	4321	TTTAAAGTTCATCAGCGCGGAGATGCCCTCCACCGAGGACCTGTTTAACTCCTGCT	4380	5461	TCAGAAAATAAGGTAGTAAATTTTGGACTCTTTTCGAGCGCTCCAAAGCGGAGGATGAG	5520
Db	4321	TTTAAAGTTCATCAGCGCGGAGATGCCCTCCACCGAGGACCTGTTTAACTCCTGCT	4380	5461	TCAGAAAATAAGGTAGTAAATTTTGGACTCTTTTCGAGCGCTCCAAAGCGGAGGATGAG	5520
Qy	4381	ATCCTCTCCCTTGGCGCCTAGTGTGGGGTGTGTGGGAGGATAGTGGTGGG	4440	5521	AGGGAAGTATCGGTTCCCGCGGAGATCTCGGAGGTCCAGGAAATTCCTCGAGCGATG	5580
Db	4381	ATCCTCTCCCTTGGCGCCTAGTGTGGGGTGTGTGGGAGGATAGTGGTGGG	4440	5521	AGGGAAGTATCGGTTCCCGCGGAGATCTCGGAGGTCCAGGAAATTCCTCGAGCGATG	5580
Qy	4441	GTGGGCGGAGGAGGGGCTGTCAGTGAAGAACCGGCTGATAGGCTTCCGTCGGG	4500	5581	CCCATATGGGACGCGCGGATTAACACCTCCACTGTTAGAGTCTCTGGAAGAACCGGAC	5640
Db	4441	GTGGGCGGAGGAGGGGCTGTCAGTGAAGAACCGGCTGATAGGCTTCCGTCGGG	4500	5581	CCCATATGGGACGCGCGGATTAACACCTCCACTGTTAGAGTCTCTGGAAGAACCGGAC	5640
Qy	4501	GGTAAACACGCTCTCCCGCAGCATATGCTGCTGAGAGCGACGCTGCAACGTTGCT	4560	5641	TACGTCCTTCCAGTGGTACACGGGTGTCCATTTCCGCGCTGCCAAGGCCCTCCGATACCA	5700
Db	4501	GGTAAACACGCTCTCCCGCAGCATATGCTGCTGAGAGCGACGCTGCAACGTTGCT	4560	5641	TACGTCCTTCCAGTGGTACACGGGTGTCCATTTCCGCGCTGCCAAGGCCCTCCGATACCA	5700
Qy	4561	CAGATCCTCTAGTCTTACCATCTAGCTGCTGAAGAGGCTTCCAGGTGGATCAAC	4620	5701	CTTCCACGAGGAGGAGGAGGAGTGTGCTGTGTCAGAAATCTACCGTGTCTTCTGCTTGGCG	5760
Db	4561	CAGATCCTCTAGTCTTACCATCTAGCTGCTGAAGAGGCTTCCAGGTGGATCAAC	4620	5701	CTTCCACGAGGAGGAGGAGGAGTGTGCTGTGTCAGAAATCTACCGTGTCTTCTGCTTGGCG	5760
Qy	4621	GAGGATGCTCCACGCGCATGCTCCGCTGCTGGCTAAGAGATGTTTGGGATGATGC	4680	5761	GAGCTCGCCACAAAGACCTTCCGCGAGCTCCGAAATCGTCCGCGCTCGACGCGGACGCA	5820
Db	4621	GAGGATGCTCCACGCGCATGCTCCGCTGCTGGCTAAGAGATGTTTGGGATGATGC	4680	5761	GAGCTCGCCACAAAGACCTTCCGCGAGCTCCGAAATCGTCCGCGCTCGACGCGGACGCA	5820
Qy	4681	ACGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAGCTCTCTGCGGAGTTGCCGGA	4740			

QY	5821	ACGGCCTCTCTGACCAAGCCCTCCGACGAGCGGACGCGGATCCGACGTTGAGTCGTAC	5880
Db	5821	ACGGCCTCTCTGACCAAGCCCTCCGACGAGCGGACGCGGATCCGACGTTGAGTCGTAC	5880
QY	5881	TCCTCCATGCCCCCTTGAAGGGGAGCGGGGATCCCGATCTCAGCGACGGTCTTGG	5940
Db	5881	TCCTCCATGCCCCCTTGAAGGGGAGCGGGGATCCCGATCTCAGCGACGGTCTTGG	5940
QY	5941	TTTACCGTAAAGCAGGAGGTAGTAGGAGCGTCTGCTGCTGCTCGATCTCTACATGG	6000
Db	5941	TTTACCGTAAAGCAGGAGGTAGTAGGAGCGTCTGCTGCTGCTCGATCTCTACATGG	6000
QY	6001	ACAGGGCCCTGATCAGCGCATCGCTGCGAGGAAACCAAGCTGCCCATCAATGCACTG	6060
Db	6001	ACAGGGCCCTGATCAGCGCATCGCTGCGAGGAAACCAAGCTGCCCATCAATGCACTG	6060
QY	6061	AGCAACTCTTTGCTCCGTACCACTTGTGACACTCGAGTCTGCTACAACTCTCGACGCAAGC	6120
Db	6061	AGCAACTCTTTGCTCCGTACCACTTGTGACACTCGAGTCTGCTACAACTCTCGACGCAAGC	6120
QY	6121	CTGCGCAGAAAGAGTCACTTTGACAGACTCGAGTCCAGCTTAAAGCTAAACTTTCTATCCGTGGAG	6180
Db	6121	CTGCGCAGAAAGAGTCACTTTGACAGACTCGAGTCCAGCTTAAAGCTAAACTTTCTATCCGTGGAG	6180
QY	6181	GTGCTCAAGAGATGAAGCGAAGCGCTCCACAGTTAAGGCTAAACTTTCTATCCGTGGAG	6240
Db	6181	GTGCTCAAGAGATGAAGCGAAGCGCTCCACAGTTAAGGCTAAACTTTCTATCCGTGGAG	6240
QY	6241	GAAAGCTGTAAGCTGACGCGCCCACTTGGCCAGATCTAAATTTGGCTATGGGCAAG	6300
Db	6241	GAAAGCTGTAAGCTGACGCGCCCACTTGGCCAGATCTAAATTTGGCTATGGGCAAG	6300
QY	6301	GACGTCGGAAACCTATCCAGCAAGCGCTTAAACACATCCGCTCCGCTGCGAGCACTTG	6360
Db	6301	GACGTCGGAAACCTATCCAGCAAGCGCTTAAACACATCCGCTCCGCTGCGAGCACTTG	6360
QY	6361	CTGGAAGACATGAGACACCAATGACACCAATCATGGCAAAATGAGGTTTCTGC	6420
Db	6361	CTGGAAGACATGAGACACCAATGACACCAATCATGGCAAAATGAGGTTTCTGC	6420
QY	6421	GTCCAAACAGAGAGGGGGCGCAAGCCAGCTCGCTTATCGTATTCACGATTTGGG	6480
Db	6421	GTCCAAACAGAGAGGGGGCGCAAGCCAGCTCGCTTATCGTATTCACGATTTGGG	6480
QY	6481	GTTCGTGTGTGCGAATAATGCGCCCTTTACGATGTGCTCCACCCCTCCCTCAGGCCGTG	6540
Db	6481	GTTCGTGTGTGCGAATAATGCGCCCTTTACGATGTGCTCCACCCCTCCCTCAGGCCGTG	6540
QY	6541	ATGGCTCTTCAATACGATTCOAATCTCTCTGACACGCGGTGAGTTCTCGTGAAT	6600
Db	6541	ATGGCTCTTCAATACGATTCOAATCTCTCTGACACGCGGTGAGTTCTCGTGAAT	6600
QY	6601	GCCTGGAAGCGAATAATGCCCTATGGCTTCGCAATATGACACCGCTGTTTGACTCA	6660
Db	6601	GCCTGGAAGCGAATAATGCCCTATGGCTTCGCAATATGACACCGCTGTTTGACTCA	6660
QY	6661	ACGGTCACTGAGATGACATCGCTGTGAGGAGTCAATCTACCAATGTTGACTTGGCC	6720
Db	6661	ACGGTCACTGAGATGACATCGCTGTGAGGAGTCAATCTACCAATGTTGACTTGGCC	6720
QY	6721	CCGGAAGCAGACAGGCCATAGGTCGCTCAGACGCGCTTTATCATCGGGGGCCCCCTG	6780
Db	6721	CCGGAAGCAGACAGGCCATAGGTCGCTCAGACGCGCTTTATCATCGGGGGCCCCCTG	6780
QY	6781	ACTAATCTTAAGGCGAAGCTGGGCTATCGCGGTGCGCGGAGCGGTGTACTGACG	6840
Db	6781	ACTAATCTTAAGGCGAAGCTGGGCTATCGCGGTGCGCGGAGCGGTGTACTGACG	6840
QY	6841	ACCAGCTGCGGTAAATACCTCTCACATGTTTACTTGAAGCGCGCTGCGGCTGTCTGCG	6900
Db	6841	ACCAGCTGCGGTAAATACCTCTCACATGTTTACTTGAAGCGCGCTGCGGCTGTCTGCG	6900

QY	6901	AAGCTCCAGGACTGCACGATGCTCGTATGCGGAGACGACCTTGTCTGTTATCTGTGAAGC	6960
Db	6901	AAGCTCCAGGACTGCACGATGCTCGTATGCGGAGACGACCTTGTCTGTTATCTGTGAAGC	6960
QY	6961	GCGGGACCCCAAGAGGACGAGCGAGCTTACGGGCCCTTACGGAGGCTATGACTAGATAC	7020
Db	6961	GCGGGACCCCAAGAGGACGAGCGAGCTTACGGGCCCTTACGGAGGCTATGACTAGATAC	7020
QY	7021	TTCTGCCCCCTCTGGGACCGCCCCAAACCAAGATACGACTTGGAGTTGATAAATCATATGC	7080
Db	7021	TTCTGCCCCCTCTGGGACCGCCCCAAACCAAGATACGACTTGGAGTTGATAAATCATATGC	7080
QY	7081	TCCTCAATGTGTACGTCGCGACGATGATCTGCGGAGCACTAGACACACTCCAGTCAAT	7140
Db	7081	TCCTCAATGTGTACGTCGCGACGATGATCTGCGGAGCACTAGACACACTCCAGTCAAT	7140
QY	7141	GACCCACCAACCCCTCTGCGGGGCTGCTGCGGAGCACTAGACACACTCCAGTCAAT	7200
Db	7141	GACCCACCAACCCCTCTGCGGGGCTGCTGCGGAGCACTAGACACACTCCAGTCAAT	7200
QY	7201	TCCTGCTAGGCAACATCATATGATGCGCCACCTTGTGGGCAAGGATGATCCTGATG	7260
Db	7201	TCCTGCTAGGCAACATCATATGATGCGCCACCTTGTGGGCAAGGATGATCCTGATG	7260
QY	7261	ACTCATTTCTTCCATCTCTCTAGCTCAGGACAACTTTGAAAAGCCCTAGATGTCAG	7320
Db	7261	ACTCATTTCTTCCATCTCTCTAGCTCAGGACAACTTTGAAAAGCCCTAGATGTCAG	7320
QY	7321	ATCTAGGGGCTGTGTACTTCCATGAGCCACTTACCTACCTCAGATCAATTAACGACTC	7380
Db	7321	ATCTAGGGGCTGTGTACTTCCATGAGCCACTTACCTACCTCAGATCAATTAACGACTC	7380
QY	7381	CATGGCTTAGCGATTTTCACTCCATGTTACTCTCCAGGTGAGATCAATAGGTTGGCT	7440
Db	7381	CATGGCTTAGCGATTTTCACTCCATGTTACTCTCCAGGTGAGATCAATAGGTTGGCT	7440
QY	7441	TCATGCTCAGGAACTTGGGCTACCGCCCTTGGGAGTCTGGAGACATCGGGCCAGAACT	7500
Db	7441	TCATGCTCAGGAACTTGGGCTACCGCCCTTGGGAGTCTGGAGACATCGGGCCAGAACT	7500
QY	7501	GTCCGCGCTAGGCTACTGTCCAGGGGGGGGCTGCCACTTGTGGCAAGTACCTCTTC	7560
Db	7501	GTCCGCGCTAGGCTACTGTCCAGGGGGGGGCTGCCACTTGTGGCAAGTACCTCTTC	7560
QY	7561	AACGCGGAGTAAAGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCGTCCAGTTGGAT	7620
Db	7561	AACGCGGAGTAAAGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCGTCCAGTTGGAT	7620
QY	7621	TTATCCAGCTGTTGCTCATGTGTGCTTACTCTCTCTCTGAGGGGTAGGCACTCAT	7680
Db	7621	TTATCCAGCTGTTGCTCATGTGTGCTTACTCTCTCTCTGAGGGGTAGGCACTCAT	7680
QY	7681	GCCGACCCGCTGTTGCTCATGTGTGCTTACTCTCTCTCTGAGGGGTAGGCACTCAT	7740
Db	7681	GCCGACCCGCTGTTGCTCATGTGTGCTTACTCTCTCTCTGAGGGGTAGGCACTCAT	7740
QY	7741	CTACTCCCCAACCAGATGAAACCGGAGCTAAACACTCCAGGCCAATAGGSCCATCTCTGTTT	7800
Db	7741	CTACTCCCCAACCAGATGAAACCGGAGCTAAACACTCCAGGCCAATAGGSCCATCTCTGTTT	7800
QY	7801	TTTCCCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTT	7860
Db	7801	TTTCCCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTT	7860
QY	7861	TTTTTCTCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTT	7920
Db	7861	TTTTTCTCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTT	7920
QY	7921	TAGCTGTGAAGGTCGCTGAGCGCTTACTGACGAGAGTGTCTGATCTAGTCTGCTCTGCG	7980
Db	7921	TAGCTGTGAAGGTCGCTGAGCGCTTACTGACGAGAGTGTCTGATCTAGTCTGCTCTGCG	7980
QY	7981	AGATCAAGT 7989	

|||||

7981 AGATCAAGT 7989

Db

RESULT 13

ABK91440

ID ABK91440 standard; DNA; 10690 BP.

XX AC

XX ABK91440;

XX DT

15-NOV-2002 (first entry)

XX DE

Hepatitis C virus vector construct pHCVNeo.17m7.

XX KW

HCV; ss; pHCVNeo.17m2; adaptive mutation; liver failure; cirrhosis;

KW hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;

XX internal ribosome entry site; IRES; NS5A; HCV replication; mutant.

XX OS

Hepatitis C virus.

OS Encephalomyocarditis virus.

OS Escherichia coli.

OS Enterobacteria phage T7.

OS Synthetic.

XX PH

Key Location/Qualifiers

FT 5'UTR

1..341

/\*tag= a

342..1181

/\*tag= b

/product= "Core-neo fusion protein"

1190..1800

/\*tag= c

/label= IRES

/note= "Internal ribosome entry site from EMCV"

1801..7758

/\*tag= d

/product= "Polyprotein"

/note= "Comprising NS3, NS4A, NS4B, NS5A and NS5B"

replace(4847,A)

/\*tag= e

replace(5243,C)

/\*tag= f

7759..7991

/\*tag= g

7992..10690

/\*tag= h

/note= "Plasmid derived sequences"

XX FT

WO200259321-A2.

XX PN

01-AUG-2002.

XX PD

16-JAN-2002; 2002MO-EP000526.

XX PF

23-JAN-2001; 2001US-0263479P.

XX PR

(RICE-) IST RICERCHIE BIOL MOLECOLARE ANGELETTI.

XX PA

De Francesco R, Migliaccio G, Paonessa G;

XX PI

WPI; 2002-599793/64.

XX DR

New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV

NS5 encoding region, or encephalomyocarditis virus (EMCV) internal

ribosome entry site (IRES) region, useful in studying HCV replication and

expression.

XX PT

Claim 16; Page; 69pp; English.

XX PS

The invention relates to nucleic acid molecules comprising altered HCV

NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)

internal ribosome entry site (IRES) region coding for one or more NS3,

NS5A, or EMCV IRES mutations, respectively. The location of the mutations

XX CC

CC

CC

CC

CC

CC

are detailed in the specification. Also included are (1) an expression vector comprising a nucleotide sequence coding for the altered nucleic acids, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell human hepatoma cell comprising the altered nucleic acids; (3) a recombinant cell produced by introducing into a human hepatoma cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus) replicon enhanced cell or which containing a functional HCV replicon; (5) an HCV replicon enhanced cells made in the method; and (6) measuring the ability of a compound to affect HCV activity. The HCV replicons and HCV replicon enhanced cells are useful in studying HCV replication and expression, and HCV and host cell interactions, producing HCV RNA and proteins, and providing a system for measuring the ability of a compound to modulate one or more HCV activities e.g. to discover drugs which may treat HCV mediated diseases such as liver failure, cirrhosis and hepatocellular carcinoma. The present sequence is an HCV based vector pHCVNeo.17 mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the HCV vector sequence appearing as ABK91412 and the information in Claim 16

XX Sequence 10690 BP; 2333 A; 3045 C; 2908 G; 2404 T; 0 U; 0 Other;

Query Match 100.0%; Score 7988.8; DB 6; Length 10690;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 7990; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCAGCCCCCGATTGGGGCGACACTCCACATAGATCACTCCCTCTGAGGAACACTG 60

DB 1 GCCAGCCCCCGATTGGGGCGACACTCCACATAGATCACTCCCTCTGAGGAACACTG 60

QY 61 TCTTCACGCAAGAAAGCGTCTAGCCATGGCTAGTATGAGTGTCTGTCAGCTCCAGGAC 120

DB 61 TCTTCACGCAAGAAAGCGTCTAGCCATGGCTAGTATGAGTGTCTGTCAGCTCCAGGAC 120

QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATGCCAG 180

DB 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATGCCAG 180

QY 181 GACGACCGGTCTCTTCTTGGATCAACCCGCTCAATGCCTGGAGATTGGCGTCCCCC 240

DB 181 GACGACCGGTCTCTTCTTGGATCAACCCGCTCAATGCCTGGAGATTGGCGTCCCCC 240

QY 241 GCGAGACTGCTAGCGGAGTAGTGTGGTCCGAAAGCCCTTGTGTAATCGCTGATAGG 300

DB 241 GCGAGACTGCTAGCGGAGTAGTGTGGTCCGAAAGCCCTTGTGTAATCGCTGATAGG 300

QY 301 GTGCTTGGAGTGCCTCCCGGAGGTCTCGTAGACCGTGCACATGAGGACGAATCCTAAC 360

DB 301 GTGCTTGGAGTGCCTCCCGGAGGTCTCGTAGACCGTGCACATGAGGACGAATCCTAAC 360

QY 361 CTCAGAGAAAACCAAGGGCGGCCATGATTGACAGATGGATTGCACGAGTTCTC 420

DB 361 CTCAGAGAAAACCAAGGGCGGCCATGATTGACAGATGGATTGCACGAGTTCTC 420

QY 421 CGGCGCTTGGTGGAGAGGCTATTTCGGCTATGACTGGGCAACAGCAATTCGCTGCT 480

DB 421 CGGCGCTTGGTGGAGAGGCTATTTCGGCTATGACTGGGCAACAGCAATTCGCTGCT 480

QY 481 CTGATGCCCGCTGTTCCGGCTGTACGCGAGGGGCGCCGGTCTTTTTCAGACCG 540

DB 481 CTGATGCCCGCTGTTCCGGCTGTACGCGAGGGGCGCCGGTCTTTTTCAGACCG 540

QY 541 ACCTGTCGGTGCCTTGAATGAACTGCGAGGACGAGCGAGCGGCTATCGTGGCTGGCA 600

DB 541 ACCTGTCGGTGCCTTGAATGAACTGCGAGGACGAGCGAGCGGCTATCGTGGCTGGCA 600

QY 601 CGACGGGCTTCTTTCGCGAGCTGTGCTCGAGTGTGCTCAGTGAAGCGGGAAGGAGTGC 660

DB 601 CGACGGGCTTCTTTCGCGAGCTGTGCTCGAGTGTGCTCAGTGAAGCGGGAAGGAGTGC 660

QY 661 TGCTATTGGCGGAAGTGCCTGCTGATCTCTCTGATCTCACTTCTCTCTGCGGAGA 720

DB 661 TGCTATTGGCGGAAGTGCCTGCTGATCTCTCTGATCTCACTTCTCTCTGCGGAGA 720

QY 721 AAGTATCCATCATGGCTGATGCAATGCGGGCTGTCATACGCTTGATCCGGCTACCTGCC 780  
 Db 721 AAGTATCCATCATGGCTGATGCAATGCGGGCTGTCATACGCTTGATCCGGCTACCTGCC 780  
 QY 781 CATTTCAGACCAAGCGAAATCGCATCCAGCGAGCACGATCTCGATGGAAGCCGGTC 840  
 Db 781 CATTTCAGACCAAGCGAAATCGCATCCAGCGAGCACGATCTCGATGGAAGCCGGTC 840  
 QY 841 TTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGGCGACAGCCGAACTGTTGC 900  
 Db 841 TTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGGCGACAGCCGAACTGTTGC 900  
 QY 901 CAGGGCTCAAGGCGCGATGCCGAGCGGAGGATCTCGTCGTGACCCATGGCGATGCTT 960  
 Db 901 CAGGGCTCAAGGCGCGATGCCGAGCGGAGGATCTCGTCGTGACCCATGGCGATGCTT 960  
 QY 961 GCTTTCGCGAATATCATGGTGGAAATGCGCGCTTTCTGGATTCATCGACTGTGGCGGC 1020  
 Db 961 GCTTTCGCGAATATCATGGTGGAAATGCGCGCTTTCTGGATTCATCGACTGTGGCGGC 1020  
 QY 1021 TGGGTGTGGCGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGGAAGAGC 1080  
 Db 1021 TGGGTGTGGCGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGGAAGAGC 1080  
 QY 1081 TTGGGCGGAATGGGCTGACCGCTTCTCGTCTTTACGGTAPCGCGCTCCGATTTGCG 1140  
 Db 1081 TTGGGCGGAATGGGCTGACCGCTTCTCGTCTTTACGGTAPCGCGCTCCGATTTGCG 1140  
 QY 1141 AGCGCATCGCCTTCTATCGCCTTTCTGACGAGTTCTTCTGAGTTTAAACAGACCAACAGC 1200  
 Db 1141 AGCGCATCGCCTTCTATCGCCTTTCTGACGAGTTCTTCTGAGTTTAAACAGACCAACAGC 1200  
 QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAACTGCTTCTGCGC 1260  
 Db 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAACTGCTTCTGCGC 1260  
 QY 1261 CGAAGCGCTTGGATAGGCGCGTGTGGCTTGTCTATATGTTATTTTCCACCATATTG 1320  
 Db 1261 CGAAGCGCTTGGATAGGCGCGTGTGGCTTGTCTATATGTTATTTTCCACCATATTG 1320  
 QY 1321 CGCTCTTTTGGCAATGTGAGGCGCGGAACTGCGCCCTGCTTCTGAGTGTGAGGAGCATTCCT 1380  
 Db 1321 CGCTCTTTTGGCAATGTGAGGCGCGGAACTGCGCCCTGCTTCTGAGTGTGAGGAGCATTCCT 1380  
 QY 1381 AGGGTCTTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGCTGTAAGGAAGCA 1440  
 Db 1381 AGGGTCTTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGCTGTAAGGAAGCA 1440  
 QY 1441 GTTCTCTGGAAGCTTCTTGAGACAAACAGCTCTGAGGACCCCTTTGCAAGGCGG 1500  
 Db 1441 GTTCTCTGGAAGCTTCTTGAGACAAACAGCTCTGAGGACCCCTTTGCAAGGCGG 1500  
 QY 1501 AACCCCCACCTGCGCAGAGTGTCTGCGGCCAAAGGACAGCGTATAGATACACT 1560  
 Db 1501 AACCCCCACCTGCGCAGAGTGTCTGCGGCCAAAGGACAGCGTATAGATACACT 1560  
 QY 1561 GCAAGGCGGCAACCCAGTCCACGTTGTGAGTTGATGTTGTAAGAGTCAAA 1620  
 Db 1561 GCAAGGCGGCAACCCAGTCCACGTTGTGAGTTGATGTTGTAAGAGTCAAA 1620  
 QY 1621 TGGCTCTCTCAAGGTTATCAACAGGGGCTGAAGGATGCCAGAGGTACCCCATGT 1680  
 Db 1621 TGGCTCTCTCAAGGTTATCAACAGGGGCTGAAGGATGCCAGAGGTACCCCATGT 1680  
 QY 1681 ATGGGATCTGATCTGGGCTCGGTGACATGCTTTACATGTTTATGTCGAGGTAAAA 1740  
 Db 1681 ATGGGATCTGATCTGGGCTCGGTGACATGCTTTACATGTTTATGTCGAGGTAAAA 1740  
 QY 1741 AACGTCTAGGCCCCGGAACCAAGGAGCGTGGTTTCTTTGAAAAACAGATAATACC 1800  
 Db 1741 AACGTCTAGGCCCCGGAACCAAGGAGCGTGGTTTCTTTGAAAAACAGATAATACC 1800  
 QY 1801 ATGGCGCTATTACGGCTACTCCCAACAGACGAGCGCTTACTTGGCTGCATCATCACT 1860

Db 1801 ATGGCGCTATTACGGCTACTCCCAACAGACGCGAGGCTTACTTGGCTGCATCATCACT 1860  
 QY 1861 AGCCTCACAGCGCGGACAGAAACAGAGTCCAGGGGAGGTCCAAAGTGTCTCCACCGCA 1920  
 Db 1861 AGCCTCACAGCGCGGACAGAAACAGAGTCCAGGGGAGGTCCAAAGTGTCTCCACCGCA 1920  
 QY 1921 ACACAACTCTTCTCGGACCTCGGTCAATGGCGTGTGTGGACTGTCTATCATGTGTGC 1980  
 Db 1921 ACACAACTCTTCTCGGACCTCGGTCAATGGCGTGTGTGGACTGTCTATCATGTGTGC 1980  
 QY 1981 GGCTCAAGAACCTTCCGCGCCCAAGGGCCCAATCAACCAATGTACACCAATGTGGAC 2040  
 Db 1981 GGCTCAAGAACCTTCCGCGCCCAAGGGCCCAATCAACCAATGTACACCAATGTGGAC 2040  
 QY 2041 CAGGACCTCGTGGCTGGCAAGCGCCCGGGCGCGTTCCTTGACACCATCACTGC 2100  
 Db 2041 CAGGACCTCGTGGCTGGCAAGCGCCCGGGCGCGTTCCTTGACACCATCACTGC 2100  
 QY 2101 GGCAGCTCGGACCTTTACTTGTGACAGGCGATGCCGATGTCAATCCGGTGGCGCGCG 2160  
 Db 2101 GGCAGCTCGGACCTTTACTTGTGACAGGCGATGCCGATGTCAATCCGGTGGCGCGCG 2160  
 QY 2161 GGCAGCAGCAGGGGAGCGCTACTCTCCCGCAGCGCGCTCTCTTGAAGGCTCTTGC 2220  
 Db 2161 GGCAGCAGCAGGGGAGCGCTACTCTCCCGCAGCGCGCTCTCTTGAAGGCTCTTGC 2220  
 QY 2221 GGCCTTCACTCTCTGCGGCTCGGGGACGCTGTGGGCTTTCGGGCTGCGGTGTGC 2280  
 Db 2221 GGCCTTCACTCTCTGCGGCTCGGGGACGCTGTGGGCTTTCGGGCTGCGGTGTGC 2280  
 QY 2281 ACCCGAGGGGTTCCGAGCGGCTGAGCTTTGACCGCTGAGTCTATGGAACCACTATG 2340  
 Db 2281 ACCCGAGGGGTTCCGAGCGGCTGAGCTTTGACCGCTGAGTCTATGGAACCACTATG 2340  
 QY 2341 CGGTCCCGGCTCTTCAAGGACAACTCGTCCCTCGCGCGCTACCGCAGACATTCAGG 2400  
 Db 2341 CGGTCCCGGCTCTTCAAGGACAACTCGTCCCTCGCGCGCTACCGCAGACATTCAGG 2400  
 QY 2401 GCCCATCTACAGCGCCCTTACTGGTAGCGGCAAGAGCACTAAGGTGCGGCTGCTATGCA 2460  
 Db 2401 GCCCATCTACAGCGCCCTTACTGGTAGCGGCAAGAGCACTAAGGTGCGGCTGCTATGCA 2460  
 QY 2461 GCCCAAGGGTATAGGTGCTTGTCTGAAACCGCTCGCGCGCAACCTAGGTTTCGG 2520  
 Db 2461 GCCCAAGGGTATAGGTGCTTGTCTGAAACCGCTCGCGCGCAACCTAGGTTTCGG 2520  
 QY 2521 GCGTATATGTAAAGGACATGGTATCGACCTTAACATCAGAACCGGGGTAAAGGACCATC 2580  
 Db 2521 GCGTATATGTAAAGGACATGGTATCGACCTTAACATCAGAACCGGGGTAAAGGACCATC 2580  
 QY 2581 ACCAGGGTGGCCCATCACTACTCCACCTATGGCAAGTTTCTTGGCGAGGTGTGC 2640  
 Db 2581 ACCAGGGTGGCCCATCACTACTCCACCTATGGCAAGTTTCTTGGCGAGGTGTGC 2640  
 QY 2641 TCTGGGCGCTTATGACATCAATATGATGATGATGATGATGATGATGATGATGATGATG 2700  
 Db 2641 TCTGGGCGCTTATGACATCAATATGATGATGATGATGATGATGATGATGATGATGATG 2700  
 QY 2701 ATCTCGGCGCTCGGACAGTCTCGACCAAGCGAGACGGCTGAGCGGCTGCTGCTG 2760  
 Db 2701 ATCTCGGCGCTCGGACAGTCTCGACCAAGCGAGACGGCTGAGCGGCTGCTGCTG 2760  
 QY 2761 CTGCGCACCGCTAGCTCTCGGGATCGGTCAACCGTGCACATCCAAACATCGAGAGGTG 2820  
 Db 2761 CTGCGCACCGCTAGCTCTCGGGATCGGTCAACCGTGCACATCCAAACATCGAGAGGTG 2820  
 QY 2821 GCTCTGTCAGCACTGAGAAATCCCTTTTATGGCAAGGCTATCCCATCGAGACCATC 2880  
 Db 2821 GCTCTGTCAGCACTGAGAAATCCCTTTTATGGCAAGGCTATCCCATCGAGACCATC 2880  
 QY 2881 AAGGGGAGGACCACTCTCTGCTTCTCAAGAGAAATGATGATGATGATGATGATGATG 2940

Db 2881 AAGGGGGAGGACCTCATTTTCTGCCATTCCAAAGAAATGTGATGAGCTCGCGCG 2940  
Qy  
2941 AAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTAACGGGGCCCTTGATGATCCGTC 3000  
Db  
2941 AAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTAACGGGGCCCTTGATGATCCGTC 3000  
Qy  
3001 ATACCAACTAGCGGAGAGCTGATGCTGTAGCAACGGAGCGCTCTAATGACGGGCTTTACC 3060  
Db  
3001 ATACCAACTAGCGGAGAGCTGATGCTGTAGCAACGGAGCGCTCTAATGACGGGCTTTACC 3060  
Qy  
3061 GCGGATTTGCATCAGTGCATCGACTGCAATACATGTGTCAACCCAGACAGTGCATTTACG 3120  
Db  
3061 GCGGATTTGCATCAGTGCATCGACTGCAATACATGTGTCAACCCAGACAGTGCATTTACG 3120  
Qy  
3121 CTGGACCCGACCTTCAACATTGAGAGACGACCGTGTGCAACAGCGGGTGTACCGTCTG 3180  
Db  
3121 CTGGACCCGACCTTCAACATTGAGAGACGACCGTGTGCAACAGCGGGTGTACCGTCTG 3180  
Qy  
3181 CAGCGGAGGAGGAGTGTGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA 3240  
Db  
3181 CAGCGGAGGAGGAGTGTGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA 3240  
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3241 GAACGGCCCTCGGCGCATGTTCCGATTCCTCGGTTCTGTGCGAGTGTATGACGGGGCTGT 3300  
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Db  
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3361 CAGGGTTCGGCTCGGAGGACCTGAGTCTGAGTCTGGAGAGCGTCTTACAGGCTC 3420  
Db  
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Qy  
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Db  
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Qy  
3481 CTGTGATGATACAGGCTGAGTGTGGCGGAGGCTCAGGCTCCACCTCCATCTGTGGAC 3540  
Db  
3481 CTGTGATGATACAGGCTGAGTGTGGCGGAGGCTCAGGCTCCACCTCCATCTGTGGAC 3540  
Qy  
3541 CAATGTGGAGTGTCTCATACGCTAAAGCTTACGCTGACGGGCGCAACGCCCTCTGCTG 3600  
Db  
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Qy  
3601 TATAGGCTGGAGCGGTTCAAAACGAGGTTACTACACACACCCCAATACCAATACATC 3660  
Db  
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Qy  
3661 ATGGATGATGTCGGCTGACCTGGAGTGTCTCAGGACCTGGGTCGTGGTAGGCGGA 3720  
Db  
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Qy  
3721 GTCCTAGCAGTCTGGCGCGTATTGCTGACACAGGAGCGTGGTCAITTTGGGCGAGG 3780  
Db  
3721 GTCCTAGCAGTCTGGCGCGTATTGCTGACACAGGAGCGTGGTCAITTTGGGCGAGG 3780  
Qy  
3781 ATCATCTTTGTCGGAAAGCCGCGCATATTCOCGACAGGAGTCTTTTACCGGAGTTC 3840  
Db  
3781 ATCATCTTTGTCGGAAAGCCGCGCATATTCOCGACAGGAGTCTTTTACCGGAGTTC 3840  
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3841 GATGATGGAAGTGTGGCTCACCTCCCTTACATCGAACAGGGAATGAGCTCGCC 3900  
Db  
3841 GATGATGGAAGTGTGGCTCACCTCCCTTACATCGAACAGGGAATGAGCTCGCC 3900  
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Db  
3901 GAAACAATTCAACAGAGGCAATCGGGTTGTGCAAAACAGCCACCAAGCAAGCGAGGCT 3960  
Qy  
3961 GCTGCTCCGTTGGTAATCCAAAGTGGGAGCCCTCGAAGCCCTTCTGGCGGAGCATATG 4020  
Db  
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Qy 4021 TGGAAATTTTCATCAGGGGATACAATATTTAGCAGGCTTGTCCACTTGTGCTGGCAACCCC 4080  
Db  
4021 TGGAAATTTTCATCAGGGGATACAATATTTAGCAGGCTTGTCCACTTGTGCTGGCAACCCC 4080  
Qy  
4081 GGGATAGCATCATGATGCAATTCACAGCTCTNTACAGCCCGCTCACCCACCAACAT 4140  
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Qy  
4141 ACCCTCTCTTTAAACATCTGGGGGATGGTGGCCGCCCAACTTGTCTCTCCAGCGCT 4200  
Db  
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Qy  
4201 GCTTCTGCTTTTGTAGCGCCGACATCGCTGGAGCGGCTGTTGGCAGCATAGAGCTTTGG 4260  
Db  
4201 GCTTCTGCTTTTGTAGCGCCGACATCGCTGGAGCGGCTGTTGGCAGCATAGAGCTTTGG 4260  
Qy  
4261 AAGTCTGTTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGCGCTGCTGGCC 4320  
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Qy  
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Db  
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Qy  
4561 CAGATCTCTCTAGTCTTACCATCACTCAGTCTGTAAGAGGCTTCAACAGTGGATCAAC 4620  
Db  
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Qy  
4621 GAGGACTCTCCAGCCCATCTCGGCTGTAAGAGATGTTTGGGATTTGGATATGC 4680  
Db  
4621 GAGGACTCTCCAGCCCATCTCGGCTGTAAGAGATGTTTGGGATTTGGATATGC 4680  
Qy  
4681 ACAGTGTGACTGATTTCAAGACCTGCTCCAGTCCAGTCTCCGCGATTTGCCGGGA 4740  
Db  
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Qy  
4741 GTCCCTTCTTCTCATGTCAAACGTTGGGTAAGAGGAGTCTGGCGGGGAGCGGATCATG 4800  
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4741 GTCCCTTCTTCTCATGTCAAACGTTGGGTAAGAGGAGTCTGGCGGGGAGCGGATCATG 4800  
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Db  
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Db  
4921 ACCAGGGCCCTTGACACGCCCTTCCCGGCGCAATTTATTTAGGGCGCTGTGGCGGGTG 4980  
Qy  
4981 GCTGCTGAGGAGTACGTGGAGTTACGCGGGTGGGGGATTTTCCACTAGTGTGCGGCAATG 5040  
Db  
4981 GCTGCTGAGGAGTACGTGGAGTTACGCGGGTGGGGGATTTTCCACTAGTGTGCGGCAATG 5040  
Qy  
5041 ACCACTGACAAAGTAAAGTGGCGGCTGAGGTTCCGGGCCCGGAAATTTCTTCAAGAGTG 5100  
Db  
5041 ACCACTGACAAAGTAAAGTGGCGGCTGAGGTTCCGGGCCCGGAAATTTCTTCAAGAGTG 5100

QY	5101	GATGGGGTCGGTGTGCACAGTACGCTCCAGCGTGCAAAACCCCTCTTACGGGAGAGGTC	5160
DB	5101		5160
QY	5161	GATGGGGTCGGTGTGCACAGTACGCTCCAGCGTGCAAAACCCCTCTTACGGGAGAGGTC	5220
DB	5161		5220
QY	5221	ACATTTCCTGGTCGGGCTCAATCAATACCTGGTTGGTTCAGAGTCCCATGCGAGCCCGAA	5280
DB	5161		5220
QY	5221	CCGGA CGTAGCAGTGCTCAGCTTCATGTCTCACCGACCCCTCCCACTATTACGGCGGAGACG	5280
DB	5221		5280
QY	5281	CGGAGCGTAGCAGTGCTCAGCTTTCATGCTCACCGACCCCTCCCACTTACGGCGGAGACG	5340
DB	5281		5340
QY	5341	GCTAAGCGTAGCCTGGCCAGGGGATCTCCCCCTCTTTCGGCCAGCTCATCAGCTTAGCCAG	5400
DB	5341		5400
QY	5401	CTGTCTGCGCTCTCCTTCAAGGCAACATGCATCTACCCGTCAATGACTCCCGGAGCGTGAC	5460
DB	5401		5460
QY	5461	CTCATTCAGGCGCAACCTCTCTGTGGCGGAGGAGATGGCGGGAAACATCACCCCGCTGGAG	5520
DB	5461		5520
QY	5521	CTCATTCAGGCGCAACCTCTCTGTGGCGGAGGAGATGGCGGGAAACATCACCCCGCTGGAG	5580
DB	5521		5580
QY	5581	TCGAAAAATAAGGTAGTAAATTTTGGACTCTTTTCGAGCCGCTCCAAGCGGAGGAGGATGAG	5640
DB	5581		5640
QY	5641	TCGAAAAATAAGGTAGTAAATTTTGGACTCTTTTCGAGCCGCTCCAAGCGGAGGAGGATGAG	5700
DB	5641		5700
QY	5701	AGGGAAGTATTCGTTCCGGCGGAGATCCTCGGAGGTCGAGGAAATTCCTTCAGCGATG	5760
DB	5701		5760
QY	5761	AGGGAAGTATTCGTTCCGGCGGAGATCCTCGGAGGTCGAGGAAATTCCTTCAGCGATG	5820
DB	5761		5820
QY	5821	AGGGAAGTATTCGTTCCGGCGGAGATCCTCGGAGGTCGAGGAAATTCCTTCAGCGATG	5880
DB	5821		5880
QY	5881	AGGGAAGTATTCGTTCCGGCGGAGATCCTCGGAGGTCGAGGAAATTCCTTCAGCGATG	5940
DB	5881		5940
QY	5941	AGGGAAGTATTCGTTCCGGCGGAGATCCTCGGAGGTCGAGGAAATTCCTTCAGCGATG	6000
DB	5941		6000
QY	6001	AGGGAAGTATTCGTTCCGGCGGAGATCCTCGGAGGTCGAGGAAATTCCTTCAGCGATG	6060
DB	6001		6060
QY	6061	AGGGAAGTATTCGTTCCGGCGGAGATCCTCGGAGGTCGAGGAAATTCCTTCAGCGATG	6120
DB	6061		6120
QY	6121	AGGGAAGTATTCGTTCCGGCGGAGATCCTCGGAGGTCGAGGAAATTCCTTCAGCGATG	6180
DB	6121		6180
QY	6181	AGGGAAGTATTCGTTCCGGCGGAGATCCTCGGAGGTCGAGGAAATTCCTTCAGCGATG	6240
DB	6181		6240

6181	GTGCTCAAGGAGATGAAGCGCAAGCGCTCCACAGTTAAGGCTTAACCTTCATCCGTGGAG	6241
QY	GAAGCCTGTAAGCTGACGCCCCACATTTGGCGCAGATCTAAATTTGGCTATGGGCAAG	6300
DB	GAAGCCTGTAAGCTGACGCCCCACATTTGGCGCAGATCTAAATTTGGCTATGGGCAAG	6300
QY	GACGTCGCGAAACCTTATCAGCAAGCCGTTAAACACATCCGCTCCGTGTCGAAGGACTTG	6360
DB	GACGTCGCGAAACCTTATCAGCAAGCCGTTAAACACATCCGCTCCGTGTCGAAGGACTTG	6360
QY	CTGGGAAGACATGAGACACCAATTTGACACACCATCATGCGCAAAAATAGAGTTTCTGC	6420
DB	CTGGGAAGACATGAGACACCAATTTGACACACCATCATGCGCAAAAATAGAGTTTCTGC	6420
QY	GTCCAAACAGAGAAGGGGGCGCGCAAGCAGCTCGCCTTATCGTATTCCACAGATTTGGGG	6480
DB	GTCCAAACAGAGAAGGGGGCGCGCAAGCAGCTCGCCTTATCGTATTCCACAGATTTGGGG	6480
QY	GTTTGTGTGTCGAGAAATAATGGCCCTTTACGATGTGTCTTCCACCTCCCTCAGGCCGTG	6540
DB	GTTTGTGTGTCGAGAAATAATGGCCCTTTACGATGTGTCTTCCACCTCCCTCAGGCCGTG	6540
QY	ATGGGCTCTTCATACGGATTCCAATACCTCTCTGGACAGCGGTGCGAGTTCTCTGTGTAAT	6600
DB	ATGGGCTCTTCATACGGATTCCAATACCTCTCTGGACAGCGGTGCGAGTTCTCTGTGTAAT	6600
QY	GCCTGGAAAGCGAAGAAATGCCCTATGGGCTTCGCATATGACACCGCGTGTTTTGACTCA	6660
DB	GCCTGGAAAGCGAAGAAATGCCCTATGGGCTTCGCATATGACACCGCGTGTTTTGACTCA	6660
QY	ACGGTCACTGAGAAATGACATCCGTTGTGAGGATCAATCTACCAATGTTGTGACTTGGCC	6720
DB	ACGGTCACTGAGAAATGACATCCGTTGTGAGGATCAATCTACCAATGTTGTGACTTGGCC	6720
QY	CCCGAAGCAGACAGGCCATAAGTGCCTCACAGAGCGGCTTTACATCGGGGCCCGCTG	6780
DB	CCCGAAGCAGACAGGCCATAAGTGCCTCACAGAGCGGCTTTACATCGGGGCCCGCTG	6780
QY	ACTAATTTCTAAAGGCGAAGACTCGCGGCTATCGCGGTGCGCGGCGAGCGGTGTACTGACG	6840
DB	ACTAATTTCTAAAGGCGAAGACTCGCGGCTATCGCGGTGCGCGGCGAGCGGTGTACTGACG	6840
QY	ACGAGCTGCGGTATACCTTCAATGTTACTTGAAGCCCGCTGCGGCCCTGTGAGAGTCGG	6900
DB	ACGAGCTGCGGTATACCTTCAATGTTACTTGAAGCCCGCTGCGGCCCTGTGAGAGTCGG	6900
QY	AAGCTTCAGGACTGACAGATGCTGATGCGGAGACGACCTTGTGCTTATCTGTCAAGC	6960
DB	AAGCTTCAGGACTGACAGATGCTGATGCGGAGACGACCTTGTGCTTATCTGTCAAGC	6960
QY	CGCGGGACCCAAAGAGCAGGCGAGCCTACGGGCTTCAACGAGGCTATGACTAGATAC	7020
DB	CGCGGGACCCAAAGAGCAGGCGAGCCTACGGGCTTCAACGAGGCTATGACTAGATAC	7020
QY	TCTGCCCGCCCTGGGACCGGCCCAACAGATACGACTTGGAGTTGATTAACATCATGCG	7080
DB	TCTGCCCGCCCTGGGACCGGCCCAACAGATACGACTTGGAGTTGATTAACATCATGCG	7080
QY	TCCTCCAATGTGTCAGTGCGGCACGATGATCTGCGAAAGGGTGTACTTCTCAACCGT	7140
DB	TCCTCCAATGTGTCAGTGCGGCACGATGATCTGCGAAAGGGTGTACTTCTCAACCGT	7140
QY	GACCCACCAACCCCTTTCGCGGGCTGCGTGGGAGACGAGCTAGACACACTCCAGTCAAT	7200
DB	GACCCACCAACCCCTTTCGCGGGCTGCGTGGGAGACGAGCTAGACACACTCCAGTCAAT	7200
QY	TCTTGGCTAGGCAACATCATGATATGCGGCCACCTTGTGGGCAAGGATGATCTGTATG	7260
DB	TCTTGGCTAGGCAACATCATGATATGCGGCCACCTTGTGGGCAAGGATGATCTGTATG	7260
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Db 7261 ACTCATTTCTTCTCCATCTTCTAGCTCAGGAACAACTTGAAGAGCCCTAGATTGTCTAG 7320  
Qy 7321 ATCTAGGGGCTGTGTACTCCATTTGAGCCACTTGACTTACCTCAGATCAATCAAGACTC 7380  
Db 7321 ATCTAGGGGCTGTGTACTCCATTTGAGCCACTTGACTTACCTCAGATCAATCAAGACTC 7380  
Qy 7381 CATGGCTTAGGCAATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGTGGCT 7440  
Db 7381 CATGGCTTAGGCAATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGTGGCT 7440  
Qy 7441 TCATGCTTCAGGAAACTTGGGGTACCGCCCTTGCGAGTCTGGAGACATCGGGCCAGAACT 7500  
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Qy 7561 AACTGGGCAAGTAAAGCAACCAAGCTCAAACTCACTCCCAATCCCGCTGCGTCCCAAGTTGGAT 7620  
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Qy 7621 TTATCCAGCTGGTTCGTGTGTTTACAGCGGGGAGACATATACAGCCCTGTCTCGT 7680  
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Db 7741 CTACTCCCCAACCGATGAACGGGGAGCTAAACACTCCAGGCCAATAGGCCATCCTGTTTT 7800  
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Db 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860  
Qy 7861 TTTTCTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 7920  
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Qy 7921 TAGCTGTGAAGGTCCTGAGCCGCTTGACTGCAGAGAGTGTGATACTGGCCCTCTCTGC 7980  
Db 7921 TAGCTGTGAAGGTCCTGAGCCGCTTGACTGCAGAGAGTGTGATACTGGCCCTCTCTGC 7980  
Qy 7981 AGATCAAGTACT 7992  
Db 7981 AGATCAAGTACT 7992

RESULT 14

ADP86271  
ID ADP86271 standard; DNA; 11313 BP.

XX AC ADP86271;

XX DT 23-SEP-2004 (first entry)

XX DE Hepatitis C virus Con-1 replicon I377/NS3-3' derived plasmid DNA, pZS10.  
XX KW Hepatitis C virus; HCV; anti-HCV agent; HCV infection; therapy; plasmid;  
XX KW ds.

XX OS Hepatitis C virus.

XX PN WO2004055216-A2.

XX PD 01-JUL-2004.

XX PF 12-DEC-2003; 2003WO-US039722.

XX PR 13-DEC-2002; 2002US-0433303P.

XX (FOXC-) FOX CHASE CANCER CENT.  
XX PI Zhu Q, Guo J, Seeger C;  
XX DR WPI; 2004-488079/46.  
XX PT New cell-line that replicates hepatitis C virus (HCV), where the cell  
XX line is selected from a non-human cell line and a human non-hepatic cell  
XX line, useful for identifying anti-HCV agents for treating HCV infections.  
XX Example III; SEQ ID NO 8; 130pp; English.  
XX The present invention provides hepatitis C virus (HCV) replication cells  
XX and cell lines derived from human non-hepatic cells or non-human cells.  
XX The invention is useful for identifying anti-HCV agents for treating HCV  
XX infections. The present sequence is hepatitis C virus Con-1 replicon  
XX CC I377/NS3-3' derived plasmid DNA.  
XX SQ Sequence 11313 BP; 2346 A; 3334 C; 3153 G; 2480 T; 0 U; 0 Other;  
XX  
XX Query Match 100.0%; Score 7988.8; DB 12; Length 11313;  
XX Best Local Similarity 100.0%; Pred. No. 0;  
XX Matches 7990; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GCCAGCCCCCGATTGGGGGCGACACTCCACATAGATFCACTCCCTGTGAGGAACACTCTG 60  
Db 1 GCCAGCCCCCGATTGGGGGCGACACTCCACATAGATFCACTCCCTGTGAGGAACACTCTG 60  
Qy 61 TCTTACGAGCAAGAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGACGCTCCAGGAC 120  
Db 61 TCTTACGAGCAAGAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGACGCTCCAGGAC 120  
Qy 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGGAAACCGGTGAGTACACCGGAATTCGCAG 180  
Db 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGGAAACCGGTGAGTACACCGGAATTCGCAG 180  
Qy 181 GAGCACCGGTCTCTTTTGGATCAACCCCGCTCAATGCTGGAGATTGGCGCGTGCCTCC 240  
Db 181 GAGCACCGGTCTCTTTTGGATCAACCCCGCTCAATGCTGGAGATTGGCGCGTGCCTCC 240  
Qy 241 GCAGACTGTAGCCGAGTAGTGTGGTTCGCAAGAGCCCTTGTGTACTGCTCTGATAGG 300  
Db 241 GCAGACTGTAGCCGAGTAGTGTGGTTCGCAAGAGCCCTTGTGTACTGCTCTGATAGG 300  
Qy 301 GTGCTTCGAGTGTCCCGGAGGTCTCGTAGACCGTGCACCATGAGCAAGATTCCTAAAC 360  
Db 301 GTGCTTCGAGTGTCCCGGAGGTCTCGTAGACCGTGCACCATGAGCAAGATTCCTAAAC 360  
Qy 361 CTCAGAGAAAAACCAAGAGGCGGCCATGATGAAAGATGGAATGGAATTCAGCAGGTTCTC 420  
Db 361 CTCAGAGAAAAACCAAGAGGCGGCCATGATGAAAGATGGAATGGAATTCAGCAGGTTCTC 420  
Qy 421 CGGCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACACACAGCAATCGGCTGCT 480  
Db 421 CGGCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACACACAGCAATCGGCTGCT 480  
Qy 481 CTGATGCGCGCTGTTCCGGCTGTGACGCGAGGGCGCCCGGTTCTTTTGTCAAGACCG 540  
Db 481 CTGATGCGCGCTGTTCCGGCTGTGACGCGAGGGCGCCCGGTTCTTTTGTCAAGACCG 540  
Qy 541 ACCTGTCCGTTGCCCTGAATGAACTGAGGAGGAGCGCGGCTATCGTGGCTGGCCA 600  
Db 541 ACCTGTCCGTTGCCCTGAATGAACTGAGGAGGAGCGCGGCTATCGTGGCTGGCCA 600  
Qy 601 CGACGGCGTTCCTTGGCAGCTGCTGCTCGACGTTGTCACTGAAGCGGGAAGGAGTCTGC 660  
Db 601 CGACGGCGTTCCTTGGCAGCTGCTGCTCGACGTTGTCACTGAAGCGGGAAGGAGTCTGC 660  
Qy 661 TGCTATTGGGCGAAGTGC CGGGGAGGATCTCTGTATCTCACTTGTCTCTCGCCGAGA 720  
Db 661 TGCTATTGGGCGAAGTGC CGGGGAGGATCTCTGTATCTCACTTGTCTCTCGCCGAGA 720

QY	721	AAGTATCCATCATGGCTGATGGAATGCGGGGCTGTCATACGCTTGATCCGGCTACCTGCC	780
Db	721	AAGTATCCATCATGGCTGATGGAATGCGGGGCTGTCATACGCTTGATCCGGCTACCTGCC	780
QY	781	CATTCCACCAACCAAGCGAATCGCATCGAGCGAGCAGCATCTCGATCGGATGGAAGCCGGTC	840
Db	781	CATTCCACCAACCAAGCGAATCGCATCGAGCGAGCAGCATCTCGATCGGATGGAAGCCGGTC	840
QY	841	TTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCGCGAATCTGTTCG	900
Db	841	TTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCGCGAATCTGTTCG	900
QY	901	CCAGGCTCAAGCGCGCATCGCGACGCGAGGATCTCGTCTGGAACCCATGCGCATGCTTC	960
Db	901	CCAGGCTCAAGCGCGCATCGCGACGCGAGGATCTCGTCTGGAACCCATGCGCATGCTTC	960
QY	961	GCTTGCCGAATATCATGGTGGAAATGCGCGCTTTTCTGGAATCATCGATGTCGGCGGC	1020
Db	961	GCTTGCCGAATATCATGGTGGAAATGCGCGCTTTTCTGGAATCATCGATGTCGGCGGC	1020
QY	1021	TGGGTGTCGGAACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGC	1080
Db	1021	TGGGTGTCGGAACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGC	1080
QY	1081	TTGGCGGCAATGCGGCTGACCGCTTCTCGTCTTTACGATATGCGCTCCCGATTCGC	1140
Db	1081	TTGGCGGCAATGCGGCTGACCGCTTCTCGTCTTTACGATATGCGCTCCCGATTCGC	1140
QY	1141	AGCGATCGCCTTCTATCGCCTTTCTGAGAGTCTTCTGAGTTTAAACAGACCAACG	1200
Db	1141	AGCGATCGCCTTCTATCGCCTTTCTGAGAGTCTTCTGAGTTTAAACAGACCAACG	1200
QY	1201	GTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCGCTTAACTGCTGCTG	1260
Db	1201	GTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCGCTTAACTGCTGCTG	1260
QY	1261	CGAGCGCTTGAATAGCGCGTGTGGTTGCTATATGTTATTTTCCACCATATTG	1320
Db	1261	CGAGCGCTTGAATAGCGCGTGTGGTTGCTATATGTTATTTTCCACCATATTG	1320
QY	1321	CGCTCTTTTGGCAATGTCAGGSCCGGAACTGCGCCCTCTCCCTCCCGCCCGCTTAACTGCTG	1380
Db	1321	CGCTCTTTTGGCAATGTCAGGSCCGGAACTGCGCCCTCTCCCTCCCGCCCGCTTAACTGCTG	1380
QY	1381	AGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAGGAAGCA	1440
Db	1381	AGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAGGAAGCA	1440
QY	1441	GTTCTCTGGAAGCTTCTTGAAGACAAACAGTCTGTAGCGACCTTTGCAAGGACGCT	1500
Db	1441	GTTCTCTGGAAGCTTCTTGAAGACAAACAGTCTGTAGCGACCTTTTGCAGGCGG	1500
QY	1501	AACCCCTCTGCGACAGTGTCTGCGGCCAAAGCCACGTCGTATAGATACACT	1560
Db	1501	AACCCCTCTGCGACAGTGTCTGCGGCCAAAGCCACGTCGTATAGATACACT	1560
QY	1561	GCAAGGCGCAACCCAGTGCACGTTGTGAGTTGGATAGTTGTGGAAGAGTCAAA	1620
Db	1561	GCAAGGCGCAACCCAGTGCACGTTGTGAGTTGGATAGTTGTGGAAGAGTCAAA	1620
QY	1621	TGGCTCTCTCAAGGATTTCAACAGGGGCTGAAGGATGCCAGAGGTACCCCATTTG	1680
Db	1621	TGGCTCTCTCAAGGATTTCAACAGGGGCTGAAGGATGCCAGAGGTACCCCATTTG	1680
QY	1681	ATGGATCTGATCTGGGSCCTCGGTGACATGCTTTTACATGTTTAGTCAGGTTAAA	1740
Db	1681	ATGGATCTGATCTGGGSCCTCGGTGACATGCTTTTACATGTTTAGTCAGGTTAAA	1740
QY	1741	AACGTCTAGGCCCCCGAACCAACCGGAGCGTGGTTTCTTTGAAACACGATAATACC	1800
Db	1741	AACGTCTAGGCCCCCGAACCAACCGGAGCGTGGTTTCTTTGAAACACGATAATACC	1800
QY	1801	ATGGCGGCTATTACGGCTACTCCCAACAGACGCGGCCTACTTGGCTGCATCACT	1860

Db	1801	ATGGCGGCTATTACGGCTACTCCCAACAGACCGGAGGCCCTACTTGGCTGCATCACT	1860
QY	1861	AGCTTCAAGCGCGGACAGGAACCAAGGTGAGAGGAGGTCCAAGTGTCTCCACCGCA	1920
Db	1861	AGCTTCAAGCGCGGACAGGAACCAAGGTGAGAGGAGGTCCAAGTGTCTCCACCGCA	1920
QY	1921	ACACATCTTTCTTGGCGACCTGCGTCAATGGGCTGTGTGGACTGTCTATCATGTGTGC	1980
Db	1921	ACACATCTTTCTTGGCGACCTGCGTCAATGGGCTGTGTGGACTGTCTATCATGTGTGC	1980
QY	1981	GGCTCAAGACCTTTGCGCGGCCCAAGGGCCCAATCACCACCAATGTACACCAATGTGGAC	2040
Db	1981	GGCTCAAGACCTTTGCGCGGCCCAAGGGCCCAATCACCACCAATGTACACCAATGTGGAC	2040
QY	2041	CAGGACCTGCTGCGGTGGAAGGGCCCGCGGGCGGCTTCTTGAACCATGACCTGC	2100
Db	2041	CAGGACCTGCTGCGGTGGAAGGGCCCGCGGGCGGCTTCTTGAACCATGACCTGC	2100
QY	2101	GGCAGTCCGACCTTTACTTGGCTCAGAGGATGCGGATGTCTATTCGGTGGCGCGG	2160
Db	2101	GGCAGTCCGACCTTTACTTGGCTCAGAGGATGCGGATGTCTATTCGGTGGCGCGG	2160
QY	2161	GGCGACAGCAGGGGAGGCTTACTCTCCCGAGGCGGCTCTCTTGAAGGCTCTTCG	2220
Db	2161	GGCGACAGCAGGGGAGGCTTACTCTCCCGAGGCGGCTCTCTTGAAGGCTCTTCG	2220
QY	2221	GGCGTCCACTGCTCTGCGGCTCGGGCAGCGTGTGGGCTCTTTCGGGCTGCGGTGC	2280
Db	2221	GGCGTCCACTGCTCTGCGGCTCGGGCAGCGTGTGGGCTCTTTCGGGCTGCGGTGC	2280
QY	2281	ACCCAGGGGTGCGAAGGCGGTGACCTTTGACCGTGCAGTCTATGGAACCACTATG	2340
Db	2281	ACCCAGGGGTGCGAAGGCGGTGACCTTTGACCGTGCAGTCTATGGAACCACTATG	2340
QY	2341	CGGTCCCGGCTCTTCAAGCAAACTCGTCCCTCGCGCGGTACCGCAGACATTCAGG	2400
Db	2341	CGGTCCCGGCTCTTCAAGCAAACTCGTCCCTCGCGCGGTACCGCAGACATTCAGG	2400
QY	2401	GCCCATCTACAGCGCCCTTACTGGTAGCGGCAAGAGCACTAAGGTGCGGTATGCA	2460
Db	2401	GCCCATCTACAGCGCCCTTACTGGTAGCGGCAAGAGCACTAAGGTGCGGTATGCA	2460
QY	2461	GCCCAAGGGTAAAGTGTCTTCTGAAACCGGTGCGCGGCGCACCTAGGTTTCGG	2520
Db	2461	GCCCAAGGGTAAAGTGTCTTCTGAAACCGGTGCGCGGCGCACCTAGGTTTCGG	2520
QY	2521	CGGTATATGCTAAGGCAACATGCTATCGACCTTAACATCAGAACCGGGTAAAGGACATC	2580
Db	2521	CGGTATATGCTAAGGCAACATGCTATCGACCTTAACATCAGAACCGGGTAAAGGACATC	2580
QY	2581	ACCAAGGTCGCCCATCAGCTATCCACTATGAGTGCAGAGTTTCTTGGCGAGTGTGC	2640
Db	2581	ACCAAGGTCGCCCATCAGCTATCCACTATGAGTGCAGAGTTTCTTGGCGAGTGTGC	2640
QY	2641	TCTGGGCGGCTATGATCATATATGATGAGTGCACATCAAAACATCGAGGAGTG	2700
Db	2641	TCTGGGCGGCTATGATCATATATGATGAGTGCACATCAAAACATCGAGGAGTG	2700
QY	2701	ATCCTGGGCTCGGACAGTCTTCTGACCAAGCGGAGACGGCTGGAGCGGCTCGTGTG	2760
Db	2701	ATCCTGGGCTCGGACAGTCTTCTGACCAAGCGGAGACGGCTGGAGCGGCTCGTGTG	2760
QY	2761	CTGCCACCGCTACGCTCGGGATCGGTCAACGTCGCCACATCAAAACATCGAGGAGTG	2820
Db	2761	CTGCCACCGCTACGCTCGGGATCGGTCAACGTCGCCACATCAAAACATCGAGGAGTG	2820
QY	2821	GCTCTGTCAGGCTGAGAAATCCCTTTTATGGAAGGATCCCTCATCGAGACCATC	2880
Db	2821	GCTCTGTCAGGCTGAGAAATCCCTTTTATGGAAGGATCCCTCATCGAGACCATC	2880
QY	2881	AAGGGGGGAGGACCTCATTTTCTGCGCTTCAAGGAAGAAATGTGATGCTGCGCG	2940



DB	6181	GTGCTCAAGAGAGATGAAGCGCAAGCGCTCCACAGTTAAGCTTAACTTCTATCCGTGGAG	6240
QY	6241	GAAAGCTCTAAGCTGAGCGCCCCACATTCGCGCCAGATCTAAATTTGGCTATGGGCAAG	6300
DB	6241	GAAGCTCTAAGCTGAGCGCCCCACATTCGCGCCAGATCTAAATTTGGCTATGGGCAAG	6300
QY	6301	GACGTCGGAACCTTATCAGCAAGCGCGTTAAACACATCCGCTCCGCTGCGAAGGACTTG	6360
DB	6301	GACGTCGGAACCTTATCAGCAAGCGCGTTAAACACATCCGCTCCGCTGCGAAGGACTTG	6360
QY	6361	CTGGAAGACACTGAGACACCAATTGACACCAACATATGCCAAATAAGTATGGTCTGCG	6420
DB	6361	CTGGAAGACACTGAGACACCAATTGACACCAACATATGCCAAATAAGTATGGTCTGCG	6420
QY	6421	GTCCAAACAGAGAAGGGGCGCAAGCCAGCTCGCCTTACGATGTGGTCTCCACCCCTCCCTCAGGCGCTG	6480
DB	6421	GTCCAAACAGAGAAGGGGCGCAAGCCAGCTCGCCTTACGATGTGGTCTCCACCCCTCCCTCAGGCGCTG	6480
QY	6481	GTTCTGTGTGCGAAGAAATGGCCCTTTACGATGTGGTCTCCACCCCTCCCTCAGGCGCTG	6540
DB	6481	GTTCTGTGTGCGAAGAAATGGCCCTTTACGATGTGGTCTCCACCCCTCCCTCAGGCGCTG	6540
QY	6541	ATGGGCTCTTCATACGGAATTCGAATCTCTCTGGAAGCGGTCGAGTTCCTGTGTAAT	6600
DB	6541	ATGGGCTCTTCATACGGAATTCGAATCTCTCTGGAAGCGGTCGAGTTCCTGTGTAAT	6600
QY	6601	GCCTGGAAGCGAAGAAATGCCCTTATGGGCTTCGCATATGACACCCGCTGTTTGACTCA	6660
DB	6601	GCCTGGAAGCGAAGAAATGCCCTTATGGGCTTCGCATATGACACCCGCTGTTTGACTCA	6660
QY	6661	ACGCTCACTCAGAAATGACATCCGCTGTTGAGGAGTCAATCTACCAATGTTGTGACTTGGCC	6720
DB	6661	ACGCTCACTCAGAAATGACATCCGCTGTTGAGGAGTCAATCTACCAATGTTGTGACTTGGCC	6720
QY	6721	CCGGAAGCCAGACAGGCCATTAAGGTGCTTACAGAGCGGCTTTACATCGGGGCCCCCTG	6780
DB	6721	CCGGAAGCCAGACAGGCCATTAAGGTGCTTACAGAGCGGCTTTACATCGGGGCCCCCTG	6780
QY	6781	ACTAATTTCTAAAGGCGAAGCTCGCGCTATCGCGGTCGCGGCGAGCGGCTACTGACG	6840
DB	6781	ACTAATTTCTAAAGGCGAAGCTCGCGCTATCGCGGTCGCGGCGAGCGGCTACTGACG	6840
QY	6841	ACCAGCTGCGGTAAATACCCCTCACAATGTAATTTGAAGCGCGCTTCGCGGCTTCGAGTGGC	6900
DB	6841	ACCAGCTGCGGTAAATACCCCTCACAATGTAATTTGAAGCGCGCTTCGCGGCTTCGAGTGGC	6900
QY	6901	AAGTTCAGAGACTGCAAGATGCTTCGTATGCGAGACGACCTTGTGCTTATCTGTGAAAGC	6960
DB	6901	AAGTTCAGAGACTGCAAGATGCTTCGTATGCGAGACGACCTTGTGCTTATCTGTGAAAGC	6960
QY	6961	GCGGGAGCCACAGAGACAGGCGGAGCTTACGGGCTTCACGGAGGCTATGACTAGATAC	7020
DB	6961	GCGGGAGCCACAGAGACAGGCGGAGCTTACGGGCTTCACGGAGGCTATGACTAGATAC	7020
QY	7021	TCTGCCCTCCCTGGGACCCGCCAAACAGAAATACGACTTCGAGTTGATAACATCATGCG	7080
DB	7021	TCTGCCCTCCCTGGGACCCGCCAAACAGAAATACGACTTCGAGTTGATAACATCATGCG	7080
QY	7081	TCTTCCAAATGTGTAGTCGCGACAGATGATCTGCGAAAGGGTGTACTATCTCCACCGT	7140
DB	7081	TCTTCCAAATGTGTAGTCGCGACAGATGATCTGCGAAAGGGTGTACTATCTCCACCGT	7140
QY	7141	GACCCACACACCCCTTCGCGGCGGCTGCGTGGGAGACGCTAGACACACTCCAGTCAAT	7200
DB	7141	GACCCACACACCCCTTCGCGGCGGCTGCGTGGGAGACGCTAGACACACTCCAGTCAAT	7200
QY	7201	TCCTGGCTAGGCAACATCATGATATGCGCCACACTTGTGGCAAGGATGATCTGTATG	7260
DB	7201	TCCTGGCTAGGCAACATCATGATATGCGCCACACTTGTGGCAAGGATGATCTGTATG	7260
QY	7261	ACTCATTTCTTCATCCTTCTAGCTCAGGAACAACCTTGAAAAAGCCCTAGATTGTGAC	7320

Db 7261 ACTCATTTCTTCTCCATCTCTTAGCTCAGAACAACTTGAAAAGCCCTAGATTGTCTAG 7320  
 QY 7321 ATCTAGGGGCGCTGTTTACTCCATTGAGCCACTTGACCTACCTCAGATCAATTCACACACTC 7380  
 Db 7321 ATCTAGGGGCGCTGTTTACTCCATTGAGCCACTTGACCTACCTCAGATCAATTCACACACTC 7380  
 QY 7381 CATGGCTTAGCGCATTTTCACTCCATAGTATTCTCTCCAGGTGAGATCAATAGGGTGGCT 7440  
 Db 7381 CATGGCTTAGCGCATTTTCACTCCATAGTATTCTCTCCAGGTGAGATCAATAGGGTGGCT 7440  
 QY 7441 TCATGGCTCAGGAACTTGGGGTACCGCCCTTCGAGTCTGAGAGATCGGGGCCAAGT 7500  
 Db 7441 TCATGGCTCAGGAACTTGGGGTACCGCCCTTCGAGTCTGAGAGATCGGGGCCAAGT 7500  
 QY 7501 GTCCGGCTAGGCTACTGTCAGGGGGGAGGGCTGCCACTTGTGCAAGTACCTCTTC 7560  
 Db 7501 GTCCGGCTAGGCTACTGTCAGGGGGGAGGGCTGCCACTTGTGCAAGTACCTCTTC 7560  
 QY 7561 AACTGGGCACTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCTCCAGTTGGAT 7620  
 Db 7561 AACTGGGCACTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCTCCAGTTGGAT 7620  
 QY 7621 TTATCCAGCTGGTTCGTGCTGTTTACAGCGGGGAGACATATATACAGCCTGTCTCGT 7680  
 Db 7621 TTATCCAGCTGGTTCGTGCTGTTTACAGCGGGGAGACATATATACAGCCTGTCTCGT 7680  
 QY 7681 GCCCGACCCCGCTGTTTCACTGCTGCTACTCTCTACTTCTGTAGGGGTAGGCATCTAT 7740  
 Db 7681 GCCCGACCCCGCTGTTTCACTGCTGCTACTCTCTACTTCTGTAGGGGTAGGCATCTAT 7740  
 QY 7741 CTACTCCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCCTGTTTT 7800  
 Db 7741 CTACTCCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCCTGTTTT 7800  
 QY 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860  
 Db 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860  
 QY 7861 TTTTCTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 7920  
 Db 7861 TTTTCTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 7920  
 QY 7921 TAGCTGTGAAGGTCCTGAGCGCTTGACTGACGAGAGTCTGATACCTGCTCTCTGTC 7980  
 Db 7921 TAGCTGTGAAGGTCCTGAGCGCTTGACTGACGAGAGTCTGATACCTGCTCTCTGTC 7980  
 QY 7981 AGATCAAGTACT 7992  
 Db 7981 AGATCAAGTACT 7992

## RESULT 15

AAD25322  
 ID AAD25322 standard; cDNA; 7989 BP.

XX AC AAD25322;

XX DT 12-MAR-2002 (first entry)

XX DE Hepatitis C virus (HCV) replBartMan/Avail cDNA.

XX KW Hepatitis C virus; HCV; transfection; infection; virus neutralisation;  
 gene therapy; vaccine; immunoprotection; hepatotropic; virucide; liver;  
 SS.

XX OS Hepatitis C virus.

XX FH Key Location/Qualifiers  
 CDS 1801..7758

XX FT /\*tag= a  
 FT /product= "HCVreplBartMan polypprotein"  
 FT 7766  
 FT misc\_feature  
 FT /\*tag= b

/note= "Nucleotide creating Avail site"

WO200189364-A2.

29-NOV-2001.

23-MAY-2001; 2001WO-US016822.

23-MAY-2000; 2000US-00576989.

(UNIW ) UNIV WASHINGTON.

Rice CM, Blight KJ;

WPI; 2002-066755/09.

P-PSDB; AAE15717.

Hepatitis C virus variants having greater transfection efficiency and  
 ability to survive subpassage, useful as a vaccine for immunizing primate  
 to the virus, comprise non-naturally occurring viral sequences.

Claim 44; Page 69-71; 174pp; English.

The invention relates to Hepatitis C virus (HCV) variants which include  
 polynucleotides comprising non-naturally occurring HCV sequence and HCV  
 variants that have a transfection efficiency and ability to survive  
 subpassage greater than HCV that have wild-type polypeptide coding  
 regions. The polynucleotides of the invention are useful for identifying  
 a cell line that is permissive for infection with HCV and detecting  
 replication of HCV in cells of the cell line. They are also useful for  
 testing a compound for anti-viral properties and for inhibiting HCV  
 infection. They are also useful for the generation of defined HCV virus  
 stocks to develop in vitro and in vivo assays for virus neutralisation,  
 attachment, penetration and entry, structure/function studies on HCV  
 proteins and RNA elements and identification of new antiviral targets, a  
 systematic survey of cell culture systems and conditions to identify  
 those that support wild-type and variant HCV RNA replication and particle  
 release, production of adaptive HCV variants capable of more efficient  
 replication in cell culture, production of HCV variants with altered  
 tissue or species tropism, establishment of alternative animal models for  
 inhibitor evaluation including those supporting HCV variant replication,  
 development of cell-free HCV replication assays, production of  
 immunogenic HCV particles for vaccination, engineering of attenuated HCV  
 derivatives as possible vaccine candidates, engineering of attenuated or  
 defective HCV derivatives for expression of heterologous gene products  
 for gene therapy and vaccine applications and for utilisation of the HCV  
 glycoproteins for targeted delivery of therapeutic agents to the liver  
 or other cell types with appropriate receptors. Vaccine comprising these  
 sequences is useful for inducing immunoprotection to HCV in a primate.  
 The present sequence is Hepatitis C virus (HCV) replBartMan/Avail cDNA

Sequence 7989 BP; 1647 A; 2369 C; 2242 G; 1731 T; 0 U; 0 Other;

Query Match 99.9%; Score 7987.4; DB 6; Length 7989;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 7988; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCAGCCCCCGATTGGGGGCGACACTCCACATAGATCACTCCCTGTGAGAACTACTG 60

Db 1 GCCAGCCCCCGATTGGGGGCGACACTCCACATAGATCACTCCCTGTGAGAACTACTG 60

QY 61 TCTTTCACGCAAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCTGTCAGGCTCCAGGAC 120

Db 61 TCTTTCACGCAAAAGCGTCTAGCCATGGCGTCTAGTATGAGTGTCTGTCAGGCTCCAGGAC 120

QY 121 CCCCCCTCCCGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGAAATGCCAG 180

Db 121 CCCCCCTCCCGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGAAATGCCAG 180

QY 181 GACGACCGGGTCTTTCTTTGGATCAACCCCGTCAATGCTCGAGATTTGGCGTGCCTCC 240

Db 181 GACGACCGGGTCTTTCTTTGGATCAACCCCGTCAATGCTCGAGATTTGGCGTGCCTCC 240

QY 241 GCAGACTGCTAGCCAGTAGTGTGGTCCGAAAGGCTTGTGTACTGCTGATAGG 300  
 DB 241 GCAGACTGCTAGCCAGTAGTGTGGTCCGAAAGGCTTGTGTACTGCTGATAGG 300  
 QY 301 GTCTTTGCGAGTCCCGGAGCTCTGTAGAGCGTGCACCATGAGCAGCAATCTTAAC 360  
 DB 301 GTCTTTGCGAGTCCCGGAGCTCTGTAGAGCGTGCACCATGAGCAGCAATCTTAAC 360  
 QY 361 CTCAAGAAAAACAAAGGCGGCCCATGATTGAACAAGATGATTGACGAGGTTCTC 420  
 DB 361 CTCAAGAAAAACAAAGGCGGCCCATGATTGAACAAGATGATTGACGAGGTTCTC 420  
 QY 421 CGGCCCTTGGGTGAGAGGCTATTCCGGCTATGACTGGGCAACAACATCCGGTGT 480  
 DB 421 CGGCCCTTGGGTGAGAGGCTATTCCGGCTATGACTGGGCAACAACATCCGGTGT 480  
 QY 481 CTGATGCCCGCTGTTCCGGCTGTACGCGAGGGGCGCCGGTCTTTTGTCAAGCCG 540  
 DB 481 CTGATGCCCGCTGTTCCGGCTGTACGCGAGGGGCGCCGGTCTTTTGTCAAGCCG 540  
 QY 541 ACCTGTCCGGTGCCTGAATGAATCAGAGCAGGCGAGCGGCTATGCTGGCTGCCA 600  
 DB 541 ACCTGTCCGGTGCCTGAATGAATCAGAGCAGGCGAGCGGCTATGCTGGCTGCCA 600  
 QY 601 CGACGGCGTTCCTTGGCGAGCTGTCTGAGTGTCTCACTGAAGCGGAAAGGACTGGC 660  
 DB 601 CGACGGCGTTCCTTGGCGAGCTGTCTGAGTGTCTCACTGAAGCGGAAAGGACTGGC 660  
 QY 661 TCGTATTGGCGAAGTCCGGGCGAGGATCTCTGTCTCATCTACCTTGTCTGCGGAGA 720  
 DB 661 TCGTATTGGCGAAGTCCGGGCGAGGATCTCTGTCTCATCTACCTTGTCTGCGGAGA 720  
 QY 721 AAGTATCCATCATGCTGATGCAATGCGGCGCTGCTACGCTTGATCGGCTACTCGC 780  
 DB 721 AAGTATCCATCATGCTGATGCAATGCGGCGCTGCTACGCTTGATCGGCTACTCGC 780  
 QY 781 CATTCGACACCAAGCGGAAACATGCAATGCGAGCAGCTACTCGGATGGAAGCGGTC 840  
 DB 781 CATTCGACACCAAGCGGAAACATGCAATGCGAGCAGCTACTCGGATGGAAGCGGTC 840  
 QY 841 TTGTCGATCAGGATCATCTGGACGAGAGCATCAGGGCTCGCGCAGCGCACTGTTGC 900  
 DB 841 TTGTCGATCAGGATCATCTGGACGAGAGCATCAGGGGCTCGCGCAGCGCACTGTTGC 900  
 QY 901 CCAGGCTCAAGCGCGCATGCCGACGCGAGGATCTCGTCTGTACCCATGCGGATGCT 960  
 DB 901 CCAGGCTCAAGCGCGCATGCCGACGCGAGGATCTCGTCTGTACCCATGCGGATGCT 960  
 QY 961 GCTTCCGGAATATCATGTTGGAATAATGCGCTTTTCTGGAATCATCGACTGTGCGCGC 1020  
 DB 961 GCTTCCGGAATATCATGTTGGAATAATGCGCTTTTCTGGAATCATCGACTGTGCGCGC 1020  
 QY 1021 TGGGTGTCGGGACCGCTATCAGGACATAGGTTGGCTACCGTGATATGCTGAAGAGC 1080  
 DB 1021 TGGGTGTCGGGACCGCTATCAGGACATAGGTTGGCTACCGTGATATGCTGAAGAGC 1080  
 QY 1081 TTGGCGGGAATGAGGCTGACCGCTTCTGCTTACGCTTACCGCTCCCGCTCCGATTCGC 1140  
 DB 1081 TTGGCGGGAATGAGGCTGACCGCTTCTGCTTACGCTTACCGCTCCCGCTCCGATTCGC 1140  
 QY 1141 AGCGATCGCCTTCTATGCGCTTCTGACAGTCTTCTGAGTCTTAAACAGACCAACAGC 1200  
 DB 1141 AGCGATCGCCTTCTATGCGCTTCTGACAGTCTTCTGAGTCTTAAACAGACCAACAGC 1200  
 QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAAAGTACTGGC 1260  
 DB 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAAAGTACTGGC 1260  
 QY 1261 CGAAGCGCTTGGAAATAGCGGCTGTGCTTGTCTATATGTTATTTCCACCATATG 1320  
 DB 1261 CGAAGCGCTTGGAAATAGCGGCTGTGCTTGTCTATATGTTATTTCCACCATATG 1320  
 QY 1321 CCGTCTTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGCTTCTTGACGAGCATCTCT 1380

DB 1321 CCGTCTTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGCTCTCTTGACGAGATCTCT 1380  
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 DB 1381 AGGGGTCTTTCCCTCTCCGCAAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCA 1440  
 QY 1441 GTTCTCTCGAAGCTTCTTGAAGACAAACAACTGTGTAGCGACCTTTGACGCGAGCGG 1500  
 DB 1441 GTTCTCTCGAAGCTTCTTGAAGACAAACAACTGTGTAGCGACCTTTGACGCGAGCGG 1500  
 QY 1501 AACCCGCCCATCTGGCGACAGGTCCTCTCGCGCAAAAGCAACGCTGTATAAGATACACCT 1560  
 DB 1501 AACCCGCCCATCTGGCGACAGGTCCTCTCGCGCAAAAGCAACGCTGTATAAGATACACCT 1560  
 QY 1561 GCAAGGCGGCAACACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAGAGTCAAA 1620  
 DB 1561 GCAAGGCGGCAACACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAGAGTCAAA 1620  
 QY 1621 TGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGGATGCCAGAAAGTACCCCATTTGT 1680  
 DB 1621 TGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGGATGCCAGAAAGTACCCCATTTGT 1680  
 QY 1681 ATGGGATCTGATCTGGGCGCTCGGTGCACATGCTTTACATGTTAGTTCGAGGTTAAAA 1740  
 DB 1681 ATGGGATCTGATCTGGGCGCTCGGTGCACATGCTTTACATGTTAGTTCGAGGTTAAAA 1740  
 QY 1741 AACGTCTAGGCCCCCGAAACACAGGGGAGTGGTTCCTTTGAAAAACACGATATACG 1800  
 DB 1741 AACGTCTAGGCCCCCGAAACACAGGGGAGTGGTTCCTTTGAAAAACACGATATACG 1800  
 QY 1801 ATGGCGCTTATTACGGCTACTTCCCAACAGAGCGGCGCTACTTTGGCTGCATCATCT 1860  
 DB 1801 ATGGCGCTTATTACGGCTACTTCCCAACAGAGCGGCGCTACTTTGGCTGCATCATCT 1860  
 QY 1861 AGCCTCACAGGCGCGGACAGAGAACAGGTCGAGGGGAGGTCACAGTGTCTCCACCGCA 1920  
 DB 1861 AGCCTCACAGGCGCGGACAGAGAACAGGTCGAGGGGAGGTCACAGTGTCTCCACCGCA 1920  
 QY 1921 ACACAAATCTTCTGGCGACCTGCTCAATGGCTGTGTGGACTGTCTATCATGCTGCC 1980  
 DB 1921 ACACAAATCTTCTGGCGACCTGCTCAATGGCTGTGTGGACTGTCTATCATGCTGCC 1980  
 QY 1981 GGCTCAAGAGCCCTTGGCGGCGCCCAAGGCGCCCAATCAACCAATGTACACCAATGTGAC 2040  
 DB 1981 GGCTCAAGAGCCCTTGGCGGCGCCCAAGGCGCCCAATCAACCAATGTGACCAATGTGAC 2040  
 QY 2041 CAGGACCTCGTGGCTGCAAGCGCCCGCGGCGCGTTCCTTCCGCTGCGCGCGGCGG 2100  
 DB 2041 CAGGACCTCGTGGCTGCAAGCGCCCGCGGCGCGTTCCTTCCGCTGCGCGCGGCGG 2100  
 QY 2101 GGCAGCTCGGACCTTACTTGGTCAAGGAGATGCGGATGTCTTCCGCTGCGCGCGGCGG 2160  
 DB 2101 GGCAGCTCGGACCTTACTTGGTCAAGGAGATGCGGATGTCTTCCGCTGCGCGCGGCGG 2160  
 QY 2161 GGCAGCAGCAGGCGGAGCTACTCTCCCGAGGCGGCTCTCTTGAAGGCTCTTCCG 2220  
 DB 2161 GGCAGCAGCAGGCGGAGCTACTCTCCCGAGGCGGCTCTCTTGAAGGCTCTTCCG 2220  
 QY 2221 GCGGCTCCACTGCTGTCGCCCTCGGGGACGCTGTGGGCACTTTTCGGCTGCGGCTGTC 2280  
 DB 2221 GCGGCTCCACTGCTGTCGCCCTCGGGGACGCTGTGGGCACTTTTCGGCTGCGGCTGTC 2280  
 QY 2281 ACCGAGGGTTCGAAAGGCGGTGACTTTGTACCCGCTCGAGTCTATGAAACCACTATG 2340  
 DB 2281 ACCGAGGGTTCGAAAGGCGGTGACTTTGTACCCGCTCGAGTCTATGAAACCACTATG 2340  
 QY 2341 CGGTCCCGGCTTTCAGGCAACTGCTGCCCTCCCGCGGTACCGCAGACATTCAGAGTG 2400  
 DB 2341 CGGTCCCGGCTTTCAGGCAACTGCTGCCCTCCCGCGGTACCGCAGACATTCAGAGTG 2400  
 QY 2401 GCCCATCTACAGCCCTTCTGTTAGGCGGCAAGGACATTAAGTGTGCGGCTGCTATGCA 2460

Db	2401	GCCATCTACAGCCCTACTGTAGGGCAAGACACTAAGGTGCGGCTGCGTATGCA	2460
Qy	2461	GCCCAAGGTATTAAGTGTCTTCTGAACCCCTCGTCCGCCCAACCTAGTTCGGG	2520
Db	2461	GCCCAAGGTATTAAGTGTCTTCTGAACCCCTCGTCCGCCCAACCTAGTTCGGG	2520
Qy	2521	GCGTATATGTCTAAGGCACATGTATCGACCTTAAACATCAGAACCGGGGTAAAGACCATC	2580
Db	2521	GCGTATATGTCTAAGGCACATGTATCGACCTTAAACATCAGAACCGGGGTAAAGACCATC	2580
Qy	2581	ACCACGGGTGCCCCCAATCAAGTACTCCACTATGCGCAAGTTCCTGCGGACGGTGTGTC	2640
Db	2581	ACCACGGGTGCCCCCAATCAAGTACTCCACTATGCGCAAGTTCCTGCGGACGGTGTGTC	2640
Qy	2641	TCTGGGGGCGCCTATGACATCATATATGTATGATGCGCACTCAACTGACTCGACCACT	2700
Db	2641	TCTGGGGGCGCCTATGACATCATATATGTATGATGCGCACTCAACTGACTCGACCACT	2700
Qy	2701	ATCTGGGCGCATCGGCACAGTCTTGGAACAAGCGGAGAGCGGTGGAGCGGCACTCGTCGTG	2760
Db	2701	ATCTGGGCGCATCGGCACAGTCTTGGAACAAGCGGAGAGCGGTGGAGCGGCACTCGTCGTG	2760
Qy	2761	CTGCCACCGCTACGCCCTCGGGATCGGTCAACCGTGCACATCCAAACATCGAGAGGTG	2820
Db	2761	CTGCCACCGCTACGCCCTCGGGATCGGTCAACCGTGCACATCCAAACATCGAGAGGTG	2820
Qy	2821	GCTCTGTCCAGCACTGAGAAATCCCTTTTATGCGCAAGCCATCCCATCGAGACCATC	2880
Db	2821	GCTCTGTCCAGCACTGAGAAATCCCTTTTATGCGCAAGCCATCCCATCGAGACCATC	2880
Qy	2881	AAGGGGGGAGGCACTCATTTCTGCGCATTCGAAGAAATGTAGTCTGCCGCG	2940
Db	2881	AAGGGGGGAGGCACTCATTTCTGCGCATTCGAAGAAATGTAGTCTGCCGCG	2940
Qy	2941	AAGCTGTCCGGCTCGGACTCAATGTCTGTAGCATATTACCGGGGCTTGTATCCGTC	3000
Db	2941	AAGCTGTCCGGCTCGGACTCAATGTCTGTAGCATATTACCGGGGCTTGTATCCGTC	3000
Qy	3001	ATACCAACTAGCGAGAGCTCATTTGCTAGCAAGCGAGCTCTAAATGACGGGCTTACC	3060
Db	3001	ATACCAACTAGCGAGAGCTCATTTGCTAGCAAGCGAGCTCTAAATGACGGGCTTACC	3060
Qy	3061	GGCGATTTGCACTCAGTGTGATCGACTGCAATACATGTGTCAACCGAGACAGTCTCAGC	3120
Db	3061	GGCGATTTGCACTCAGTGTGATCGACTGCAATACATGTGTCAACCGAGACAGTCTCAGC	3120
Qy	3121	CTGAGACCGCACTTCAACATTTAGAGAGAGAGCCGTGCGCAAGAGCGGCTGTCAGCTCG	3180
Db	3121	CTGAGACCGCACTTCAACATTTAGAGAGAGAGCCGTGCGCAAGAGCGGCTGTCAGCTCG	3180
Qy	3181	CAGCGGCGAGGACAGTGTGGGCGAGGATGGGCAATTTACAGTTTGTGACTCCAGGA	3240
Db	3181	CAGCGGCGAGGACAGTGTGGGCGAGGATGGGCAATTTACAGTTTGTGACTCCAGGA	3240
Qy	3241	GAAAGGGCTCTGGGCATGTTCGATTCCTCGGTTCTGTGCGAGTGTCTATGACCGGGCTGT	3300
Db	3241	GAAAGGGCTCTGGGCATGTTCGATTCCTCGGTTCTGTGCGAGTGTCTATGACCGGGCTGT	3300
Qy	3301	GCTTGGTACAGACTCAGCGCCGCGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACA	3360
Db	3301	GCTTGGTACAGACTCAGCGCCGCGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACA	3360
Qy	3361	CCAGGGTTCGCGCTCTGCCAGGACCATCTGGAGTTCTGGAGAGCGTCTTACAGGCTTC	3420
Db	3361	CCAGGGTTCGCGCTCTGCCAGGACCATCTGGAGTTCTGGAGAGCGTCTTACAGGCTTC	3420
Qy	3421	ACCCACATAGAGCCCATTTCTTGTCCAGACTAAGAGGCGAGGAGACAATTCGCCCTAC	3480
Db	3421	ACCCACATAGAGCCCATTTCTTGTCCAGACTAAGAGGCGAGGAGACAATTCGCCCTAC	3480
Qy	3481	CTGGTAGCATACAGGCTACGGTGTGCGCCAGGGGCTCAGGGCTCCACCTCCATCGTGGAC	3540
Db	3481	CTGGTAGCATACAGGCTACGGTGTGCGCCAGGGGCTCAGGGCTCCACCTCCATCGTGGAC	3540
Qy	3541	CRAATCTGGAAGTGTCTCATACGGCTAAAGCCTAACGCTGACCGGGCCAAAGCCCTGCTG	3600
Db	3541	CRAATCTGGAAGTGTCTCATACGGCTAAAGCCTAACGCTGACCGGGCCAAAGCCCTGCTG	3600
Qy	3601	TATAGCTGAGAGCCGTTCAAAACGAGGTCTACCAACACACACACCCCAATACATC	3660
Db	3601	TATAGCTGAGAGCCGTTCAAAACGAGGTCTACCAACACACACACCCCAATACATC	3660
Qy	3661	ATGSCATGATGTGCGCTGACCTGAGGTGCTCAACAGCACCTGGTGTGTTAGGCGGA	3720
Db	3661	ATGSCATGATGTGCGCTGACCTGAGGTGCTCAACAGCACCTGGTGTGTTAGGCGGA	3720
Qy	3721	GTCTTAGCAGCTCTGCGCGGTATGCTTCAACAGGAGCGTGTGTTAGGCGGAGG	3780
Db	3721	GTCTTAGCAGCTCTGCGCGGTATGCTTCAACAGGAGCGTGTGTTAGGCGGAGG	3780
Qy	3781	ATCATCTTGTCCGGAAGCGGCGCATCATTTCCGACAGGGAATGCTTTACCGGAGTTC	3840
Db	3781	ATCATCTTGTCCGGAAGCGGCGCATCATTTCCGACAGGGAATGCTTTACCGGAGTTC	3840
Qy	3841	GATGAGATGAAGTGCCTCACACCTCCCTTATCATCGAAACAGGGAATGCACTCGCC	3900
Db	3841	GATGAGATGAAGTGCCTCACACCTCCCTTATCATCGAAACAGGGAATGCACTCGCC	3900
Qy	3901	GAACAATTTCAACAGAGGCAATCGGTTGCTGCAACAGCCACCAAGAGCGGAGGCT	3960
Db	3901	GAACAATTTCAACAGAGGCAATCGGTTGCTGCAACAGCCACCAAGAGCGGAGGCT	3960
Qy	3961	GCTGCTCCGCTGTTGGAATCCAGTGGCGGACCTCGAAGCTTCTGGGCGAAGCATATG	4020
Db	3961	GCTGCTCCGCTGTTGGAATCCAGTGGCGGACCTCGAAGCTTCTGGGCGAAGCATATG	4020
Qy	4021	TGGAATTTTCATCAGCGGGATCAATATTTAGCAGGCTTGTTCATCTGCTGGCAACCCC	4080
Db	4021	TGGAATTTTCATCAGCGGGATCAATATTTAGCAGGCTTGTTCATCTGCTGGCAACCCC	4080
Qy	4081	GCGATAGCATCAGTGTGGATTCACAGCCTCTATACAGCCCGCTCACACCCCAACAT	4140
Db	4081	GCGATAGCATCAGTGTGGATTCACAGCCTCTATACAGCCCGCTCACACCCCAACAT	4140
Qy	4141	ACCTCTCTGTTTACATCTCTGGGGGATGGGTGGCGCCCAACTTGTCTCTCCAGCGCT	4200
Db	4141	ACCTCTCTGTTTACATCTCTGGGGGATGGGTGGCGCCCAACTTGTCTCTCCAGCGCT	4200
Qy	4201	GCTTCTGCTTTCGTAGGCGCGGATCGTGGAGCGGCTGTTGGCAGCATAGGCTTGGG	4260
Db	4201	GCTTCTGCTTTCGTAGGCGCGGATCGTGGAGCGGCTGTTGGCAGCATAGGCTTGGG	4260
Qy	4261	AAGTGTCTGTGGATATTTTGGCAGGTTATGGAGAGGGGTGGCAGGCGCTCGTGCC	4320
Db	4261	AAGTGTCTGTGGATATTTTGGCAGGTTATGGAGAGGGGTGGCAGGCGCTCGTGCC	4320
Qy	4321	TTTAAAGTCTAGCGGCGAGATGCCCTCCACCGAGGACCTGGTTAACTCTCCCTGCT	4380
Db	4321	TTTAAAGTCTAGCGGCGAGATGCCCTCCACCGAGGACCTGGTTAACTCTCCCTGCT	4380
Qy	4381	ATCCTCTCCCTGCGCGCTTAGTCTGCGGGTCTGTGTCGAGCGGATCTGGTCTGGGAC	4440
Db	4381	ATCCTCTCCCTGCGCGCTTAGTCTGCGGGTCTGTGTCGAGCGGATCTGGTCTGGGAC	4440
Qy	4441	GTGGGCGCAGGGGAGGGGCTGTGAGTGTGAACCGGCTGATAGCGTTCGTTGCGGG	4500
Db	4441	GTGGGCGCAGGGGAGGGGCTGTGAGTGTGAACCGGCTGATAGCGTTCGTTGCGGG	4500
Qy	4501	GGTACACAGCTCTCCCGACGACATGCTGTGCTGAGAGCGCTGACAGCGTGTCACT	4560
Db	4501	GGTACACAGCTCTCCCGACGACATGCTGTGCTGAGAGCGCTGACAGCGTGTCACT	4560
Qy	4561	CAGATCTCTCTAGTCTTTACCATCACTCAGTGTGTGAAGAGGCTTCAACAGTGTGATAC	4620
Db	4561	CAGATCTCTCTAGTCTTTACCATCACTCAGTGTGTGAAGAGGCTTCAACAGTGTGATAC	4620

QY 4621 GAGGACTGCTCCAGCCATGCTCCGCTCGTGGCTAAAGATGTTTGGATTTGGATATGC 4680  
DB 4621 GAGGACTGCTCCAGCCATGCTCCGCTCGTGGCTAAAGATGTTTGGATTTGGATATGC 4680  
QY 4681 ACGGTGTTGACTGATTTCAAGACTTGGCTCAGTCCAGCTCTGCGCGATTTGCCGGA 4740  
DB 4681 ACGGTGTTGACTGATTTCAAGACTTGGCTCAGTCCAGCTCTGCGCGATTTGCCGGA 4740  
QY 4741 GTCCCTCTTCTCTCATGTCACAGTGGGTACAGGGAGTCTGCGGGGCGACGGCATCATG 4800  
DB 4741 GTCCCTCTTCTCTCATGTCACAGTGGGTACAGGGAGTCTGCGGGGCGACGGCATCATG 4800  
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DB 4801 CAAACACCTGCCCCATTTGGAGCACAGATCACCGGACATGTGAAAAACGGTTTCCATGAG 4860  
QY 4861 ATCTGTGGGCTTAGACCTGTAGTAACTGATGAGTGGCATGGAACAATTCCTCAATTAACGGGTAC 4920  
DB 4861 ATCTGTGGGCTTAGACCTGTAGTAACTGATGAGTGGCATGGAACAATTCCTCAATTAACGGGTAC 4920  
QY 4921 ACCACGGGCTGTCACGCTCCGCGGCGCCAAATTTATCTAGGGGCTGTGGGGGTG 4980  
DB 4921 ACCACGGGCTGTCACGCTCCGCGGCGCCAAATTTATCTAGGGGCTGTGGGGGTG 4980  
QY 4981 GCTGTGAGGAGTACGTGGAGTTACGGGGTGGGGATTTCCACTACGTGACGGGCATG 5040  
DB 4981 GCTGTGAGGAGTACGTGGAGTTACGGGGTGGGGATTTCCACTACGTGACGGGCATG 5040  
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DB 5041 ACCACTGACAGTAAAGTCCCGTGTAGGTTCCGGGCCCGAAATTTCTTCAAGAAAGT 5100  
QY 5101 GATGGGTGCGGTGTCACAGGTACGCTCCAGCGTGCACACCTCTCTAGCGGAGAGGTC 5160  
DB 5101 GATGGGTGCGGTGTCACAGGTACGCTCCAGCGTGCACACCTCTCTAGCGGAGAGGTC 5160  
QY 5161 ACATTTCTGGTCCGGCTCAATCAATACCTGGTGGGTACAGCTCCCATGCGAGCCCGAA 5220  
DB 5161 ACATTTCTGGTCCGGCTCAATCAATACCTGGTGGGTACAGCTCCCATGCGAGCCCGAA 5220  
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DB 5221 CCGGAGTAGAGTGTCTCTTCATGCTCAGGACCCCTCCCATGCGGCGAGAGC 5280  
QY 5281 GCTAAGCGTAGGCTGCGGAGGATCTCCCTCTCTGCGGAGTCTCATGCTAGCCAG 5340  
DB 5281 GCTAAGCGTAGGCTGCGGAGGATCTCCCTCTCTGCGGAGTCTCATGCTAGCCAG 5340  
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DB 5341 CTGTCTGCGCTTCTTGAAGGCAACATGCACTACCCGCTCATGCTCCCGGAGCGTGCAC 5400  
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DB 5401 CTCATCGAGGCAACCTCTGTGGGCGGAGAGATGGGGGGAACATCACCCGCTGGAG 5460  
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DB 5461 TCAGAAATTAAGTATGATTTTGGACTCTTTGAGCGGCTCCAGCGGAGGAGATGAG 5520  
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DB 5521 AGGGAAGTATCCGTTCCGCGGAGATCTCTGCGAGGTCCAGGAAATTCCTCGAGCGATG 5580  
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DB 5701 CCTCCACGGAAGAGAGCGGTTCTCTGTTCAGAACTCTACCGTGTCTTCTGCTTGGCG 5760  
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DB 5761 GAGCTCGGCAACAAAGACCTTTGGGCAAGTCTCGTGGGCGCTGCAAGCGGCAAGCA 5820  
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DB 5821 ACGGCTCTCTCTGACAGCCCTCCGACGACGCGGAGTCCGAGCTTCTGAGTCTGATC 5880  
QY 5881 TCTTCATCTCCCTCTTGGGGGAGCGGGGATCCCGATCTCTCAGCGACGGGTCTGG 5940  
DB 5881 TCTTCATCTCCCTCTTGGGGGAGCGGGGATCCCGATCTCTCAGCGACGGGTCTGG 5940  
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DB 5941 TCTACCGTAAGCGAGGAGCTAGTGAGGACGTCTGCTGCTCGATGCTCTACATGG 6000  
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DB 6061 AGCAACTCTTTGCTCCGTCAACCAACTTTGCTTATGCTTACAACTCTCGAGCGCAAGC 6120  
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DB 6121 CTGCGGCAAGAAAGGTCACTTTGACAGATGTCAGAGTCTTGGACGACCACTACCGGAC 6180  
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DB 6301 GAGCTCGGAAAGCTATCAGGAGCGGTAAACCACTCCGCTCGTGTGGAGAGACTG 6360  
QY 6361 CTGGAAGACACTGACACCACTTACACCACTATCGGCAAAATAAGAGTCTTCTG 6420  
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QY 6781 ACTAATTTAAAGGCGAAGACTGCGGCTTATCGCGCTGCGCGAGCGGCTGACTGAGC 6840

